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OM nucleic - nucleic search, using sw model

Run on: September 24, 2005, 12:51:21 ; Search time 2359 Seconds
(without alignments)
11045.342 Million cell updates/sec

Title: US-10-021-657-7

Perfect score: 3897
Sequence: 1 gaattccaagcagcgcctt.....gctgagtaacgacgaattc 3897

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 7400704 seqs, 3343079526 residues

Total number of hits satisfying chosen parameters: 14801408

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA:*

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26: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3897	100.0	3897	13	US-10-021-657-7
2	3897	100.0	3897	16	US-10-412-000-7
3	1429.2	36.7	1941	20	US-10-425-115-266
4	1378.4	35.4	1906	13	US-10-021-657-1
5	1378.4	35.4	1906	16	US-10-412-000-1
6	1092	28.0	1092	13	US-10-021-657-5
7	1092	28.0	1092	16	US-10-412-000-5

8	1083.8	27.8	1898	19	US-10-767-701-13826	Sequence 13826, A
9	268.4	6.9	494	13	US-10-021-657-3	Sequence 3, Appl1
10	268.4	6.9	494	16	US-10-412-000-3	Sequence 3, Appl1
11	263	6.7	267	13	US-10-021-657-6	Sequence 6, Appl1
12	263	6.7	267	16	US-10-412-000-6	Sequence 6, Appl1
13	224.6	5.8	342	20	US-10-425-115-87794	Sequence 87794, A
14	214.6	5.5	330	19	US-10-437-963-51459	Sequence 51459, A
15	181	4.6	444	19	US-10-437-963-75572	Sequence 75572, A
16	164.2	4.2	1807	18	US-10-425-114-23429	Sequence 23429, A
17	164.2	4.2	1833	20	US-10-425-115-110678	Sequence 110678, A
18	160.8	4.1	1611	19	US-10-437-963-93941	Sequence 93941, A
19	154.2	4.0	825	18	US-10-425-114-35451	Sequence 35451, A
20	154.2	4.0	1008	20	US-10-425-115-174414	Sequence 174414, A
21	151.8	3.9	1907	19	US-10-437-963-19259	Sequence 19259, A
22	151.6	3.9	1617	17	US-10-260-238-1236	Sequence 1236, Ap
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24	147	3.8	4937	17	US-10-437-963-89896	Sequence 89896, A
25	146.4	3.8	854	17	US-10-260-238-4619	Sequence 4619, Ap
26	145.4	3.7	1951	20	US-10-425-115-147739	Sequence 147739, Ap
27	145.2	3.7	726	19	US-10-767-701-4908	Sequence 4908, Ap
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31	143.8	3.7	1947	18	US-10-425-114-28465	Sequence 28465, A
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35	137.8	3.5	1527	17	US-10-260-238-422	Sequence 422, Ap
36	137.6	3.5	1431	19	US-10-437-963-26802	Sequence 26802, A
37	137.4	3.5	1548	19	US-10-437-963-89328	Sequence 89328, A
38	136.6	3.5	604	17	US-10-260-238-3255	Sequence 3255, Ap
39	136.6	3.5	1500	19	US-10-437-963-89894	Sequence 89894, A
40	136.2	3.5	614	19	US-10-437-963-80085	Sequence 80085, A
41	136	3.5	1949	19	US-10-437-963-26803	Sequence 26803, A
42	133.4	3.4	1820	19	US-10-767-701-13757	Sequence 13757, A
43	132.4	3.4	444	17	US-10-260-238-5268	Sequence 5268, Ap
44	131.8	3.4	1764	19	US-10-437-963-10148	Sequence 10148, A
45	131	3.4	1548	19	US-10-437-963-26804	Sequence 26804, A

ALIGNMENTS

RESULT 1
US-10-021-657-7
; Sequence 7, Application US/10021657
; Publication No. US20020083483A1
; GENERAL INFORMATION:
; APPLICANT: ALBERTSEN, MARC C.
; APPLICANT: FOX, TIM
; APPLICANT: HUFFMAN, GARY
; APPLICANT: TRIMMELL, MARY
; TITLE OF INVENTION: NUCLEOTIDE SEQUENCES MEDIATING MALE FERTILITY AND
; TITLE OF INVENTION: METHOD OF USING SAME
; FILE REFERENCE: 1146
; CURRENT APPLICATION NUMBER: US/10/021,657
; CURRENT FILING DATE: 2001-12-14
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 3897
; TYPE: DNA
; ORGANISM: Zea mays
US-10-021-657-7

Query Match 100.0%; Score 3897; DB 13; Length 3897;
Best local Similarity 100.0%; Pred. No. 0;
Matches 3897; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 1 GAATTCGAAGCAGGCGCTTGTAGAGAGAGTGTGATGACATCGCGGAAATGACT 60

QY	61	GCGRCTGAGAACACGCTGAGGGGTTCCAGGATGCGAATGCGTATGGCCTAG	120
Db	61	GGGTCTGAGAACACGCTGAGGGGTTCCAGGATGCGAATGCGTATGGCCTAG	120
QY	121	AGGTGAGGACAAAGGTGATGAGGATTTGGAAGGCAACTATGCGAATTGTGTGAAGGC	180
Db	121	AGGTGAGGACAAAGGTGATGAGGATTTGGAAGGCAACTATGCGAATTGTGTGAAGGC	180
QY	181	ACGCAATGAGATCTATTCAGACTTACATGGAATGCCGCAAGAAATTGAACCTTTAGA	240
Db	181	ACGCAATGAGATCTATTCAGACTTACATGGAATGCCGCAAGAAATTGAACCTTTAGA	240
QY	241	TTTGTATCTGTCACTCTACTTTTATTCCTGTGGGCAACTTCATAGGCTCATGTT	300
Db	241	TTTGTATCTGTCACTCTACTTTTATTCCTGTGGGCAACTTCATAGGCTCATGTT	300
QY	301	AATCATGATATGATGATTTATTCAGCAAAATTTCTGTTGTTTGAATTTAATATGTG	360
Db	301	AATCATGATATGATGATTTATTCAGCAAAATTTCTGTTGTTTGAATTTAATATGTG	360
QY	361	GGGTGAGACGATTTAATATTCATCATGAGACTTATCTTCAATGCTCTGATTTTGG	420
Db	361	GGGTGAGACGATTTAATATTCATCATGAGACTTATCTTCAATGCTCTGATTTTGG	420
QY	421	TTTCAGATCATTTCTTTCAGTGTTCAGAAATTTTCTCAGTTTGTTCATGTAATTTTGG	480
Db	421	TTTCAGATCATTTCTTTCAGTGTTCAGAAATTTTCTCAGTTTGTTCATGTAATTTTGG	480
QY	481	AAGTAGGTTCTTAAATTTTCAATTATATGCTCTTTCTTAACATGACATGCAATGA	540
Db	481	AAGTAGGTTCTTAAATTTTCAATTATATGCTCTTTCTTAACATGACATGCAATGA	540
QY	541	CTTTTCACTTTGGGTTCACAAAATTGACTCACAGAAACAAATTCATTTTGGGTTACA	600
Db	541	CTTTTCACTTTGGGTTCACAAAATTGACTCACAGAAACAAATTCATTTTGGGTTACA	600
QY	601	AATTCCTCTTCAGAGTATATCTTTTCACTTGAATGTCAATGATGGAACAGAAATGGCT	660
Db	601	AATTCCTCTTCAGAGTATATCTTTTCACTTGAATGTCAATGATGGAACAGAAATGGCT	660
QY	661	CAGTTTTTAAGGAACAATGACAGATTTCAATTTCAGAACTCTTTCTGTTGGTTGAGTTT	720
Db	661	CAGTTTTTAAGGAACAATGACAGATTTCAATTTCAGAACTCTTTCTGTTGGTTGAGTTT	720
QY	721	CAGACTTTTGTGACCAAGCTGATGATCACAATCTTGTTCAAAGTCTGATTAACGAA	780
Db	721	CAGACTTTTGTGACCAAGCTGATGATCACAATCTTGTTCAAAGTCTGATTAACGAA	780
QY	781	ACTGGCACTCCTAATTGATATTAATAAAGATTAATAACAGTATCAGATATCTAATTTTC	840
Db	781	ACTGGCACTCCTAATTGATATTAATAAAGATTAATAACAGTATCAGATATCTAATTTTC	840
QY	841	TTGTGTGCAAGTCACAAAAGGAACACAAAGGCTAAGCTCTTCACTTGTTCGGAAGTTA	900
Db	841	TTGTGTGCAAGTCACAAAAGGAACACAAAGGCTAAGCTCTTCACTTGTTCGGAAGTTA	900
QY	901	GCTCAGGACACCAATATGATGAAGAATCTTAAATTTGGGCTCACACAAAGATGTCTC	960
Db	901	GCTCAGGACACCAATATGATGAAGAATCTTAAATTTGGGCTCACACAAAGATGTCTC	960
QY	961	TCTCAGGTTGGGGGGTCCCTAAGTTGTGTATGACATATACCAATATATCACTTAACA	1020
Db	961	TCTCAGGTTGGGGGGTCCCTAAGTTGTGTATGACATATACCAATATATCACTTAACA	1020
QY	1021	ACCCATTCATATCATATCATATCAATACATGATTCATCACTTGTATGACTGAACTCTTCAATCA	1080
Db	1021	ACCCATTCATATCATATCATATCAATACATGATTCATCACTTGTATGACTGAACTCTTCAATCA	1080
QY	1081	AGAGACCATGGAAGGAGCTCAATCAAGCGGCGAGGCAATTCGCAATTTCTTCCACATAG	1140
Db	1081	AGAGACCATGGAAGGAGCTCAATCAAGCGGCGAGGCAATTCGCAATTTCTTCCACATAG	1140
QY	1141	CAGGGCTTCACAAATGATCATGGGCTCTCTGTGTGTCTCTCATGATCTCTGTGTACGA	1200

Db	1141	CAGGGCTCAAGTAATCGCGCTTCTCTGGTGTCTCTAATGAAATCTTGATCCAGA	1200
Qy	1201	GGTGAGCTTAGGAAGAGAAAGGCCGAGATCATGGCAATCATCGGTGCAACGGTGG	1260
Db	1201	GGTGAGCTTAGGAAGAGAAAGGCCGAGATCATGGCAATCATCGGTGCAACGGTGG	1260
Qy	1261	AGCAGCTGAGGAACCTACCAACCGAATGCACTGGCTGTGCGGGTACTGTACACGGACA	1320
Db	1261	AGCAGCTGAGGAACCTACCAACCGAATGCACTGGCTGTGCGGGTACTGTACACGGACA	1320
Qy	1321	GGAACGTGACCCGTGCAATGCGCTTCACTTCTTCAACCTTACATGCTGACCCGGTGAAATG	1380
Db	1321	GGAACGTGACCCGTGCAATGCGCTTCACTTCTTCAACCTTACATGCTGACCCGGTGAAATG	1380
Qy	1361	TCGAGCATGTCTTCAAGACTTACCTTACCAATTAACCCCAAGTAAATGACTGAACTCAC	1440
Db	1361	TCGAGCATGTCTTCAAGACTTACCTTACCAATTAACCCCAAGTAAATGACTGAACTCAC	1440
Qy	1441	TGATGTTCAGTCTTCGGAAATCAGAGCTGAAAGCTGAATGGAATGTGCTGAAACCGGTG	1500
Db	1441	TGATGTTCAGTCTTCGGAAATCAGAGCTGAAAGCTGAATGGAATGTGCTGAAACCGGTG	1500
Qy	1501	TAGGGAATCGTGTACAGATCTCTCATGAGACGTGCTCTCGGTGACCGCATCTTCAAGCC	1560
Db	1501	TAGGGAATCGTGTACAGATCTCTCATGAGACGTGCTCTCGGTGACCGCATCTTCAAGCC	1560
Qy	1561	GACGGCGAGCTGTGAGAGGAAGACAGGAAGACGGCGAGTTTCAGTGGCGCTCCAGAAC	1620
Db	1561	GACGGCGAGCTGTGAGAGGAAGACAGGAAGACGGCGAGTTTCAGTGGCGCTCCAGAAC	1620
Qy	1621	CTGAGGGATTTCAAGCGCATTTGTGTGAGAGAGTACTCCCTGAAGCTGTGCGGTATACTG	1680
Db	1621	CTGAGGGATTTCAAGCGCATTTGTGTGAGAGAGTACTCCCTGAAGCTGTGCGGTATACTG	1680
Qy	1661	AGCCAGGATTCAGAGGCAAGGCAAAAGTGTGTGACATGAGGTGAGATTCATCTGCTCCCTTGC	1740
Db	1661	AGCCAGGATTCAGAGGCAAGGCAAAAGTGTGTGACATGAGGTGAGATTCATCTGCTCCCTTGC	1740
Qy	1741	CATTGCCAATGAGCAATTTCCAACTTGACACAGAGAGCTACCTTGCGCATTCAGAACT	1800
Db	1741	CATTGCCAATGAGCAATTTCCAACTTGACACAGAGAGCTACCTTGCGCATTCAGAACT	1800
Qy	1801	TTAATCATGAGATGACGCTGACCTTCATCTGCAAGGTGTGGGTTGGGGGTCAAGATCGGAC	1860
Db	1801	TTAATCATGAGATGACGCTGACCTTCATCTGCAAGGTGTGGGTTGGGGGTCAAGATCGGAC	1860
Qy	1861	GCTGTCGCGGAGATCTCCCGCGAGAACAGCTTCGACAGGTGTGGGTTGGGGGTCAAGATCGGAC	1920
Db	1861	GCTGTCGCGGAGATCTCCCGCGAGAACAGCTTCGACAGGTGTGGGTTGGGGGTCAAGATCGGAC	1920
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Db	1921	CGTCAAGCTGTGGTTCATCGAACCCGCTGTGGCGCATCAAGAGTTCCTTCAACGTGGGTC	1980
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Qy	2041	CCGAGAGAGGCGAGATCGTCAGAGGCGCGGAGCGAGCAAGAGAAAGGTACTGTG	2100
Db	2041	CCGAGAGAGGCGAGATCGTCAGAGGCGCGGAGCGAGCAAGAGAAAGGTACTGTG	2100
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Db	2161	ATTATATATCCGTGTGACTTGTGAGGCAAAATTTAAATGGGCAATGAGACGACATCC	2220
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Db	2221	TGTCAACGGTTTCAATGAGCTAGGCGAGGCGGCGACGACGGCGGCGCTTTCGGGAGCGACA	2280

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Db 2341 CGGTGTGTGGTTCAACGACATGGCCATGTCCACCGGAGCGTGGCGGAGAGAGTGGGCC 2400
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Db 2521 TCCCTCACTTACGACAGGCTCGGCGAGAGTGGTCTTACCTCCACGCGCTGGGTCAACGAGACG 2580
Qy 2581 TCCGCTGTACCCCGCGCTCTTCAAGGTGAGCGCGCGGACGACGCGACCTTCGCTCCAGA 2640
Db 2581 TCCGCTGTACCCCGCGCTCTTCAAGGTGAGCGCGCGGACGACGCGACCTTCGCTCCAGA 2640
Qy 2641 GCAACAGATGAGTGAATGAGTGAACCTGAAATGCAATGCAATGCACTTGGCGCGCGGAGAC 2700
Db 2641 GCAACAGATGAGTGAATGAGTGAACCTGAAATGCAATGCAATGCACTTGGCGCGCGGAGAC 2700
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Db 3001 GGGGACCCGGTGAATGCGGATGATGACATCTCTTCAATGCGGCGACGCGCTCAAGTTC 3060
Qy 3061 CGGCTCTTGAAGGCGGCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 3120
Db 3061 CGGCTCTTGAAGGCGGCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 3120
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Db 3121 AAAATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3180
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Db 3181 CTTTAAAACTCGGTGGGCTTTCGAAACCAACCAATCACTAAGTTTGTACTTACTC 3240
Qy 3241 CTGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 3300
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Db 3301 CGGATGCTTCCGGGACCTTTTGGAGACATTAATGACAGGCGTGGTGAAGAAAGGCTTC 3360

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Db 3361 TTCTGGGCGGAAGTTTGGGTTCAAGTCTGGCGGCTTTTGAACGAGAAAGGTTGG 3420
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Db 3421 AAGGATCTGAACCTTGAACCGAAGAAATGCTTGGAAATATGCTGATCGGGCGGGCC 3480
Qy 3481 GTCACTCGGATGACGACAAAGCCCAACAGAGTGAAGAGGAAAGCTTTGGAGTTGG 3540
Db 3481 GTCACTCGGATGACGACAAAGCCCAACAGAGTGAAGAGGAAAGCTTTGGAGTTGG 3540
Qy 3541 AGACACTTCGAGACCCCTGGGCGCTCGGAGAGTCACTTTCGCTCTGCTGCTGG 3600
Db 3541 AGACACTTCGAGACCCCTGGGCGCTCGGAGAGTCACTTTCGCTCTGCTGCTGG 3600
Qy 3601 TGGCGGACCGGCGCGCGCGCTCGTGTTCACCAATCCGCGCGCGGACGCGTTCG 3660
Db 3601 TGGCGGACCGGCGCGCGCGCGCTCGTGTTCACCAATCCGCGCGCGGACGCGTTCG 3660
Qy 3661 GTACAAACCTTCATCGGCGGCGCGCGGAGTGAACAGCCCGGAGCGCGTATACAT 3720
Db 3661 GTACAAACCTTCATCGGCGGCGCGCGGAGTGAACAGCCCGGAGCGCGTATACAT 3720
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Db 3841 AGAATGAGAGACAAACCAAGGTTAGATGAAATAGCTAGTAAACAGCAATTC 3897

RESULT 2
US-10-412-000-7
; Sequence 7, Application US/10412000
; Publication No. US2003018269A1
; GENERAL INFORMATION:
; APPLICANT: ALBERTSEN, MARC C.
; APPLICANT: FOX, TIM
; APPLICANT: HUFFMAN, GARY
; APPLICANT: TRIMBLE, MARY
; TITLE OF INVENTION: NUCLEOTIDE SEQUENCES MEDIATING MALE FERTILITY AND
; FILE REFERENCE: METHOD OF USING SAME
; CURRENT APPLICATION NUMBER: US/10/412,000
; CURRENT FILING DATE: 2003-04-11
; PRIOR APPLICATION NUMBER: US/09/670,153
; PRIOR FILING DATE: 2001-06-11
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; TYPE: DNA
; ORGANISM: Zea mays
US-10-412-000-7

Query Match 100.0%; Score 3897; DB 16; Length 3897;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3897; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAATTCGAAGCGAGCCCTTGTAGCAGAGATGTTGCTGATGATGATGATGATGATGATGAT 60
Db 1 GAATTCGAAGCGAGCCCTTGTAGCAGAGATGTTGCTGATGATGATGATGATGATGATGAT 60
Qy 61 GCGTGTGAGAGCAACGCTGAGGGGTTCCAGGGATGAGCAATGGCTATGGCAATCGGCTAG 120
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QY 361 GGGTGAACGGATTAAATATCATCATGAGAGCTTTATCTTCATGCTCTTGAATTTGG 420
DB 361 GGGTGAACGGATTAAATATCATCATGAGAGCTTTATCTTCATGCTCTTGAATTTGG 420
QY 421 TTTCAATCATTTCTTCAAGTGTCAACAAGAAATTTCTCACTTGGTCCATGTAATTTTG 480
DB 421 TTTCAATCATTTCTTCAAGTGTCAACAAGAAATTTCTCACTTGGTCCATGTAATTTTG 480
QY 481 AAGTGAAGTCTTAAATTTCAATTAATGCTCTTCTTCTTCTAGACTAGCACTGCATGA 540
DB 481 AAGTGAAGTCTTAAATTTCAATTAATGCTCTTCTTCTTCTAGACTAGCACTGCATGA 540
QY 541 CTTTTCACCTTGGGTTCACAAAATTAAGTCAACAAGAAACAAATTCATTTTGGGTTCA 600
DB 541 CTTTTCACCTTGGGTTCACAAAATTAAGTCAACAAGAAACAAATTCATTTTGGGTTCA 600
QY 601 AATTCTCTTCAAGAGTATCTTTTCACTTGAACCTGTCAATGATATGGAACAAGAAATGGCT 660
DB 601 AATTCTCTTCAAGAGTATCTTTTCACTTGAACCTGTCAATGATATGGAACAAGAAATGGCT 660
QY 661 CAGTTTTTAAAGAACATGATGATGATTCATTTCAAGAACTCTTCTGTTGGTGTGAGTT 720
DB 661 CAGTTTTTAAAGAACATGATGATGATTCATTTCAAGAACTCTTCTGTTGGTGTGAGTT 720
QY 721 CAGACTTTTGTACCAAGCTGATGATCACAATTAATCTGTTCCAAAGCTGATTAACGAA 780
DB 721 CAGACTTTTGTACCAAGCTGATGATCACAATTAATCTGTTCCAAAGCTGATTAACGAA 780
QY 781 ACTGGAATCTCTTAATTTGATTAATAAAGAAATTAATACGATATCAATCTTCTTTC 840
DB 781 ACTGGAATCTCTTAATTTGATTAATAAAGAAATTAATACGATATCAATCTTCTTTC 840
QY 841 TTGGTTGGCAGATCACAAAAAGGAAACAAGAGCTACCTCTACTTGTTCGGAGTTA 900
DB 841 TTGGTTGGCAGATCACAAAAAGGAAACAAGAGCTACCTCTACTTGTTCGGAGTTA 900
QY 901 GGTGAGGACACCAATATGAATGAAGAAATCTTAATTTGGGTTCAACAAGATTTGCTC 960
DB 901 GGTGAGGACACCAATATGAATGAAGAAATCTTAATTTGGGTTCAACAAGATTTGCTC 960
QY 961 TCTCGAGGTTGGGGGGTCCCTTAAGTTGTGATGAAATCCCAATTAATCACTTAACA 1020
DB 961 TCTCGAGGTTGGGGGGTCCCTTAAGTTGTGATGAAATCCCAATTAATCACTTAACA 1020
QY 1021 ACCCAATCCATGCTACATATCATATGATTCATCTTGTAGATGAGACCTTCATCA 1080
DB 1021 ACCCAATCCATGCTACATATCATATGATTCATCTTGTAGATGAGACCTTCATCA 1080
QY 1081 AGAGCAACATGAGAGAAAGCTCAATCAAGCGCGGAGCGCATGCGCAATCTTCCACTAG 1140
DB 1081 AGAGCAACATGAGAGAAAGCTCAATCAAGCGCGGAGCGCATGCGCAATCTTCCACTAG 1140
QY 1141 CAGGGGCTCAAGATCATGCGGCTCTCTGTTGTCTCTCATGATGATCTGGTCCAGA 1200
DB 1141 CAGGGGCTCAAGATCATGCGGCTCTCTGTTGTCTCTCATGATGATCTGGTCCAGA 1200

QY 1201 GGTGAGCTCTGAGGAACAGAAAGGCCGAGATCATAGCCAGTCAATCGGTCAACGGTTGG 1260
DB 1201 GGTGAGCTCTGAGGAACAGAAAGGCCGAGATCATAGCCAGTCAATCGGTCAACGGTTGG 1260
QY 1261 AGCAGCTGAGGAATTAACAACCGGATGACAGACTGTGTGGGTAATCTGTCAAGGACA 1320
DB 1261 AGCAGCTGAGGAATTAACAACCGGATGACAGACTGTGTGGGTAATCTGTCAAGGACA 1320
QY 1321 GGAAGTGAACGGTGCACATGCGGTTCACTTCTTAACCTAATCGCTGACCGGGTGAATG 1380
DB 1321 GGAAGTGAACGGTGCACATGCGGTTCACTTCTTAACCTAATCGCTGACCGGGTGAATG 1380
QY 1381 TCGAGATGTCTCTCAAGACTAATCACTTCAACCAATTAACCCCAAGGTAATAGACTGA 1440
DB 1381 TCGAGATGTCTCTCAAGACTAATCACTTCAACCAATTAACCCCAAGGTAATAGACTGA 1440
QY 1441 TGAATTTCACTTTCGGAATCAAGAGCTGAAGAGTGAATGAAATGCTGAAACCGTG 1500
DB 1441 TGAATTTCACTTTCGGAATCAAGAGCTGAAGAGTGAATGAAATGCTGAAACCGTG 1500
QY 1501 TTAGGAAATGATGACAAATCCATCAATGACGATGCTCTCGGTGAAGGCACTTCAAGG 1560
DB 1501 TTAGGAAATGATGACAAATCCATCAATGACGATGCTCTCGGTGAAGGCACTTCAAGG 1560
QY 1561 GACGCGAGCTGTGAG 1620
DB 1561 GACGCGAGCTGTGAG 1620
QY 1621 CTGAGGAATTTCAAGGCTATGTGTTCAGAGATATCTCCCTGAAGCTGTGGGTATCTG 1680
DB 1621 CTGAGGAATTTCAAGGCTATGTGTTCAGAGATATCTCCCTGAAGCTGTGGGTATCTG 1680
QY 1681 AGCGAGGATTCAGAGGCGAGGAAAGTGTGACATGCAAGGATGATCACTGCTCCCTTGC 1740
DB 1681 AGCGAGGATTCAGAGGCGAGGAAAGTGTGACATGCAAGGATGATCACTGCTCCCTTGC 1740
QY 1741 CATTCGCAATGAGAGATTTCAACCTGAGACAGAGAGCTACCTTCCGATTCAGGAAT 1800
DB 1741 CATTCGCAATGAGAGATTTCAACCTGAGACAGAGAGCTACCTTCCGATTCAGGAAT 1800
QY 1801 TTAATGAGATGACGCTGAACTCCATCTGCAAGTGTGGGTTCCGAGTGAATCGGCAC 1860
DB 1801 TTAATGAGATGACGCTGAACTCCATCTGCAAGTGTGGGTTCCGAGTGAATCGGCAC 1860
QY 1861 GCTGTGCGGAGATCTCCCGAGAACAGCTTGGCGAGAGGCTTCGATGCGCGCAATCAT 1920
DB 1861 GCTGTGCGGAGATCTCCCGAGAACAGCTTGGCGAGAGGCTTCGATGCGCGCAATCAT 1920
QY 1921 CGTCAAGCTGCGGATTCATGACCCGCTGTGGCGCATCAAGAGTTCCTTCAAGTGGGTC 1980
DB 1921 CGTCAAGCTGCGGATTCATGACCCGCTGTGGCGCATCAAGAGTTCCTTCAAGTGGGTC 1980
QY 1981 AGAGGCTCTCTAGCGCAGAGCATCAAGTCTGTGACGAGTTCACTTACAGCTGATCCG 2040
DB 1981 AGAGGCTCTCTAGCGCAGAGCATCAAGTCTGTGACGAGTTCACTTACAGCTGATCCG 2040
QY 2041 CCGAGGAAGGCGAGATGATGAGGCGCGGCGAGCGGCGCAACAGAGAAAGTACGTC 2100
DB 2041 CCGAGGAAGGCGAGATGATGAGGCGCGGCGAGCGGCGCAACAGAGAAAGTACGTC 2100
QY 2101 ACATGACGTGTTCAATCTTCAATCTGATTCATGCTGTGTGGCGGAGATGACCTGATCT 2160
DB 2101 ACATGACGTGTTCAATCTTCAATCTGATTCATGCTGTGTGGCGGAGATGACCTGATCT 2160
QY 2161 ATTATATATCCGTGTGATCTTGTGAGGACAAATTAATAATGAGATGAAAGCAGCATTC 2220
DB 2161 ATTATATATCCGTGTGATCTTGTGAGGACAAATTAATAATGAGATGAAAGCAGCATTC 2220
QY 2221 TGTCAAGTTCATGAGCTTACGAGGCTGAGGCGGCGAGAGAGAGAGAGAGAGAGAG 2280
DB 2221 TGTCAAGTTCATGAGCTTACGAGGCTGAGGCGGCGAGAGAGAGAGAGAGAGAGAGAG 2280
QY 2281 AGAGCTCCGAGAGCTGTGTCTCAATCTTGTGATGCGCGGCGGAGACAGAGCGGAGAGA 2340

Db	2281	AGAGCTCCGGGACGTGGTGGCTCAACTTCGTGATGCGCGCGGGACACGACGGGACGA	2340
Qy	2341	CGCTGTCCGTGGTTCACGACCAATGGCCATGTGCCACCCGGACGTGGCCGAGAAGCTGGCC	2400
Db	2341	CGCTGTCCGTGGTTCACGACCAATGGCCATGTGCCACCCGGACGTGGCCGAGAAGCTGGCC	2400
Qy	2401	GGAGCTGTGCGCTTCGAGGCGGAGCGCGCGGAGAGAGCGCTCGCGCTCGTCCCT	2460
Db	2401	GGAGCTGTGCGCTTCGAGGCGGAGCGCGCGGAGAGAGCGCTCGCGCTCGTCCCT	2460
Qy	2461	GGCGGGGGCTGACCGCCGACGACAGAGGGTTTCGCCGCCCGCTGGCGGCAATTCCGGGCC	2520
Db	2461	GGCGGGGGCTGACCGCCGACGACAGAGGGTTTCGCCGCCCGCTGGCGGCAATTCCGGGCC	2520
Qy	2521	TCCTCACTTACGACAGACCTCGGCGAAGCTGGTCTACCTCAGCGCTGGCTACCGAGACG	2580
Db	2521	TCCTCACTTACGACAGACCTCGGCGAAGCTGGTCTACCTCAGCGCTGGCTACCGAGACG	2580
Qy	2581	TCGGCTGTACCCCGCGCTCCCTCAGGTGAGCGCGCCGACACGCACTTCGGTCCAGA	2640
Db	2581	TCGGCTGTACCCCGCGCTCCCTCAGGTGAGCGCGCCGACACGCACTTCGGTCCAGA	2640
Qy	2641	GCAACGCAATGCATGTGATGGACCTGGAATGCAATGCAATGCACTTGGCGCGCGCGAGAC	2700
Db	2641	GCAACGCAATGCATGTGATGGACCTGGAATGCAATGCAATGCACTTGGCGCGCGCGAGAC	2700
Qy	2701	CCCAAGGGGATCTCGAGAGACGACGTGTGCGGACCGGACGAGAGAGAGGGCGCGGG	2760
Db	2701	CCCAAGGGGATCTCGAGAGACGACGTGTGCGGACCGGACGAGAGAGAGGGCGCGGG	2760
Qy	2761	ATGTGACGTACGTGCCCTCACTCGATGGGCGGATGAGATCAACTGGGGCGCCGACGCG	2820
Db	2761	ATGTGACGTACGTGCCCTCACTCGATGGGCGGATGAGATCAACTGGGGCGCCGACGCG	2820
Qy	2821	GCGAGCTTCGGCGCGGAGCGGTGATCAACGAGATGGCGGTTCCGCAACGCGTCCCG	2880
Db	2821	GCGAGCTTCGGCGCGGAGCGGTGATCAACGAGATGGCGGTTCCGCAACGCGTCCCG	2880
Qy	2881	TTCAAGTTCAGGGGGTTCCAGGGGGGCGGAGAGATGCGCTGGGGCAAGGACTCGGCTAC	2940
Db	2881	TTCAAGTTCAGGGGGTTCCAGGGGGGCGGAGAGATGCGCTGGGGCAAGGACTCGGCTAC	2940
Qy	2941	CTGCAAGTGAAGATGCGCTGGCCACTCTCTTGGCGTCTTACAGCTTCCGCTCTGGAG	3000
Db	2941	CTGCAAGTGAAGATGCGCTGGCCACTCTCTTGGCGTCTTACAGCTTCCGCTCTGGAG	3000
Qy	3001	GGGCAACCGGTTGCAGTACCGATGATGACATCTCTTCATGGCGCAACGCGCTCAAGGTC	3060
Db	3001	GGGCAACCGGTTGCAGTACCGATGATGACATCTCTTCATGGCGCAACGCGCTCAAGGTC	3060
Qy	3061	CGCGTCTTCAGGGCGCTGTGATGTTCATGCGCAATTTGGGATTCATCCGCTTAATCTT	3120
Db	3061	CGCGTCTTCAGGGCGCTGTGATGTTCATGCGCAATTTGGGATTCATCCGCTTAATCTT	3120
Qy	3121	AAATTTGCAATGCAATGATGAAGGAAAGGATGGGTTTCATTTGGTGGCTTGAAG	3180
Db	3121	AAATTTGCAATGCAATGATGAAGGAAAGGATGGGTTTCATTTGGTGGCTTGAAG	3180
Qy	3181	CTTTAAAACTCCGTCCGCTCTTGGCAACCAACATCACTAAGTGTTTGTACTCTACTC	3240
Db	3181	CTTTAAAACTCCGTCCGCTCTTGGCAACCAACATCACTAAGTGTTTGTACTCTACTC	3240
Qy	3241	CTCAGTGAAGTGAAGTACGACGATPACAGTTTCATCATATATATATATCTCTTCTTCG	3300
Db	3241	CTCAGTGAAGTGAAGTACGACGATPACAGTTTCATCATATATATATATCTCTTCTTCG	3300
Qy	3301	CGGATGTCTTCCCGGACCTTTTGGAGACATTTACTGACAGCGCGTGTGAAAAAGGCTTC	3360
Db	3301	CGGATGTCTTCCCGGACCTTTTGGAGACATTTACTGACAGCGCGTGTGAAAAAGGCTTC	3360
Qy	3361	TTCTGCGGCGAAGTTTGGGTTCAAGAGTCTTGGCGTCTTTCAGACAGAAAAAGGTTGG	3420

Db	3361	TTCTGCGCGGAAGTTTGGGTTCAAGATCTTGCGCTCTTTGCAGCAAGAAAAAGTTTGG	3420
QY	3421	AAGGATCTGAACCCCTGAACCCGAAATGGCTTCGAAATATGCTCCGATCGGGCGGGCC	3480
Db	3421	AAGGATCTGAACCCCTGAACCCGAAATGGCTTCGAAATATGCTCCGATCGGGCGGGCC	3480
QY	3481	GTCACTCGGGATGACGACAGCCCAAGACAGTGAAGCGAAGCATCTTTGAGTTTGG	3540
Db	3481	GTCACTCGGGATGACGACAGCCCAAGACAGTGAAGCGAAGCATCTTTGAGTTTGG	3540
QY	3541	AGACACTCTCGGACCCCTCGCGGCTCCGCGAGCTCATCTTGCGCTCTCTGTCTGTCCG	3600
Db	3541	AGACACTCTCGGACCCCTCGCGGCTCCGCGAGCTCATCTTGCGCTCTCTGTCTGTCCG	3600
QY	3601	TGGCGGACCGGCGCCCGCGCTCGTGTTCGACCAATCCGCGGCCGACCGGTTGGT	3660
Db	3601	TGGCGGACCGGCGCCCGCGCTCGTGTTCGACCAATCCGCGGCCGACCGGTTGGT	3660
QY	3661	GTACAACACCTCATCCGCGGCGCGCGAGTACACGCCCGGAGCGCGTATACAT	3720
Db	3661	GTACAACACCTCATCCGCGGCGCGCGAGTACACGCCCGGAGCGCGTATACAT	3720
QY	3721	CTATTAATCATGATGTATTGTACTTTATTTTCAACGGCCTTAAACAACATATTTTATG	3780
Db	3721	CTATTAATCATGATGTATTGTACTTTATTTTCAACGGCCTTAAACAACATATTTTATG	3780
QY	3781	GTAACACAGTTTCAAAATTTGACCAAAATTTAAACAGGCAACCGGTAGCTAAACATAG	3840
Db	3781	GTAACACAGTTTCAAAATTTGACCAAAATTTAAACAGGCAACCGGTAGCTAAACATAG	3840
QY	3841	AGAAATGAGAGCAACCCCAAGGTTAGAGATGAATTAAGCTGATGAACGACGAAATTC	3897
Db	3841	AGAAATGAGAGCAACCCCAAGGTTAGAGATGAATTAAGCTGATGAACGACGAAATTC	3897
RESULT 3			
US-10-425-115-266/c			
; Sequence 266, Application US/10425115			
; Publication No. US20040214272A1			
GENERAL INFORMATION:			
; APPLICANT: La Rosa, Thomas J.			
; APPLICANT: Kovallik, David K.			
; APPLICANT: Zhou, Yihua			
; APPLICANT: Cao, Yongwei			
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With			
; TITLE OF INVENTION: Plates			
; FILE REFERENCE: 38-21(53222)B			
; CURRENT APPLICATION NUMBER: US/10/425.115			
; CURRENT FILING DATE: 2003-04-28			
; NUMBER OF SEQ ID NOS: 369326			
; SEQ ID NO 266			
; LENGTH: 1941			
; TYPE: DNA			
; ORGANISM: Zea mays			
; FEATURE:			
; OTHER INFORMATION: Clone ID: MRT4577_100246C.1			
US-10-425-115-266			
Query Match 36.7%; Score 1429.2; DB 20; Length 1941;			
Best Local Similarity 82.5%; Pred. No. 0;			
Matches 1882; Conservative 0; Mismatches 13; Indels 385; Gaps 6;			
QY	1042	TACATAGATCATCATCTTTGATGACTGAGCCCTTCATGAGAGCAACATGAGGAAGCTC	1101
Db	1938	TACATAGATCATCATCTTTGATGACTGAGCCCTTCATGAGAGCAACATGAGGAAGCTC	1879
QY	1102	ACATCAGCGCGGACGCGCATCGCATTTTCCCACTAGCAGGGGCTCAACATGATCTG	1161
Db	1878	ACCTCAGCGCGGACGCGCATCGCATTTTCCCACTAGCAGGGGCTCAACATGATCTG	1819
QY	1162	CGCTCTCTGTTGTCTCTTCATGAGATCTGTGTCAGAGGTGAGGCTGAGGAAGCAG	1221
Db	1818	CGCTCTCTGTTGTCTCTTCATGAGATCTGTGTCAGAGGTGAGGCTGAGGAAGCAG	1759


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QY 2348 GTGGTTCACGACATGAGCCATGTCACCCGAGAGTGGCGGCGGAGCT 2407
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    999 GTGGTTCACGACATGAGCCATGTCACCCGAGAGTGGCGGCGGAGCT 1058
QY 2408 GTGCGGCTTCGAGCGGAGCGCGCGGAGAGGCGTGCCTGTCGCGCGG 2467
    |||||
    1059 GTGCGGCTTCGAGCGGAGCGCGCGGAGAGGCGTGCCTGTCGCGCGG 1118
QY 2468 CGCTGACGCCGAGACAGAGCGCTTCGCGCGCGGAGAGTGGCGGCGCT 2527
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    1119 CGCTGACGCCGAGACAGAGCGCTTCGCGCGCGGAGAGTGGCGGCGCT 1178
QY 2528 CTACGACGCGCTTCGAGCGGAGCTGCTACCTCAAGCGCTGCTGACGAGAG 2587
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    1179 CTACGACGCGCTTCGAGCGGAGCTGCTACCTCAAGCGCTGCTGACGAG 1238
QY 2588 GTACCCCGCGCTTCGAGCGGAGCGCGCGGAGAGCTGCTGCTGACGAG 2647
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    1239 GTACCCCGCGCTTCGAGCGGAGCGCGCGGAGAGCTGCTGCTGACGAG 1254
QY 2648 ATGACGAGTGAAGCTGAAATGCAATGACATGCACTTGGCGCGCGGAGAG 2707
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    1255 -----CAGAGACCCCAAGG 1267
QY 2708 GGATCCCTGAGAGAGAGAGTGGCTGCGCGGAGAGAGAGAGAGAGAGAGTGA 2767
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    1268 GGATCCCTGAGAGAGAGAGTGGCTGCGCGGAGAGAGAGAGAGAGAGTGA 1327
QY 2768 CGTACGCTGCTTACTGATGAGGCGGAGTGAAGTGAAGTGGGCGCGGAGAG 2827
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    1328 CGTACGCTGCTTACTGATGAGGCGGAGTGAAGTGAAGTGGGCGCGGAGAG 1387
QY 2828 TCGGCGCGGAGCGGAGTGAAGAGAGTGGCGGCTTGGCGAGAGCGGCTTCA 2887
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    1388 TCGGCGCGGAGCGGAGTGAAGAGAGTGGCGGCTTGGCGAGAGCGGCTTCA 1447
QY 2888 TCACGCGGCTTCAAGGCGGCGGAGAGTGGCTGCGGAGAGAGTGGCTTCA 2947
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    1448 TCACGCGGCTTCAAGGCGGCGGAGAGTGGCTGCGGAGAGAGTGGCTTCA 1507
QY 2948 TGAAGATGAGCGCTGAGCATCTCTTGGCGCTTCTCAAGCTTCCGCTGAGAG 3007
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    1508 TGAAGATGAGCGCTGAGCATCTCTTGGCGCTTCTCAAGCTTCCGCTGAGAG 1567
QY 3008 CGGTGAGTACCGCATGATGACATCTCTTCAAGTGGCGAGCGCTTCAAGTCC 3067
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    1568 CGGTGAGTACCGCATGATGACATCTCTTCAAGTGGCGAGCGCTTCAAGTCC 1627
QY 3068 CTAGGCGCGCTGATGATGATGAGATTTG-----GGATATCATCCCGCTTAA 3117
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    1628 CTAGGCGCGCTGATGATGATGAGATTTG-----GGATATCATCCCGCTTAA 1687
QY 3118 -----TTAAAAATTTGATGATGATGATGATGATGATGATGATGATGAT 3163
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    1688 AAATAACGCTCGGCTTAAATTTGATGATGATGATGATGATGATGATGATGAT 1747
QY 3164 TGGTGGCTTGGCTTAAAGCTTAAAGCTTAAAGCTTAAAGCTTAAAGCTTAA 3223
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    1748 TGGTGGCTTGGCTTAAAGCTTAAAGCTTAAAGCTTAAAGCTTAAAGCTTAA 1807
QY 3224 TGGTGGCTTGGCTTAAAGCTTAAAGCTTAAAGCTTAAAGCTTAAAGCTTAA 3283
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    1808 TGGTGGCTTGGCTTAAAGCTTAAAGCTTAAAGCTTAAAGCTTAAAGCTTAA 1867
QY 3284 TTAATCTCTTCTTCTT 3297
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    1868 TTAATCTCTTCTTCTT 1881

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RESULT 6
 US-10-021-657-5
 ; Sequence 5, Application US/10021657

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; Publication No. US20020083483A1
; GENERAL INFORMATION:
; APPLICANT: ALBERTSEN, MARC C.
; APPLICANT: FOX, TIM
; APPLICANT: HUFFMAN, GARY
; APPLICANT: TRIMBLE, MARY
; TITLE OF INVENTION: NUCLEOTIDE SEQUENCES MEDIATING MALE FERTILITY AND
; TITLE OF INVENTION: METHOD OF USING SAME
; FILE REFERENCE: 1148
; CURRENT APPLICATION NUMBER: US/10/021,657
; CURRENT FILING DATE: 2001-12-14
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 1092
; TYPE: DNA
; ORGANISM: Zea mays
; US-10-021-657-5

Query Match      28.0%; Score 1092; DB 13; Length 1092;
Best Local Similarity 100.0%; Pred. No. 9,2e-291;
Matches 1092; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAAATCCAGAGAGAGCGCTTGTAGCAGAGAGTGTGCTGATGAGTGGCGGAGATGAGT 60
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    1 GAAATCCAGAGAGAGCGCTTGTAGCAGAGAGTGTGCTGATGAGTGGCGGAGATGAGT 60
DB 1 GAAATCCAGAGAGAGCGCTTGTAGCAGAGAGTGTGCTGATGAGTGGCGGAGATGAGT 60
QY 61 GCGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 120
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    61 GCGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 120
DB 61 GCGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 120
QY 121 AGGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 180
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    121 AGGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 180
DB 121 AGGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 180
QY 181 AGCATATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 240
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    181 AGCATATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 240
DB 181 AGCATATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 240
QY 241 TTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 300
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    241 TTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 300
DB 241 TTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 300
QY 301 AATCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 360
    |||||
    301 AATCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 360
DB 301 AATCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 360
QY 361 GGGTGAAGAGAGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 420
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    361 GGGTGAAGAGAGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 420
DB 361 GGGTGAAGAGAGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 420
QY 421 TTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 480
    |||||
    421 TTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 480
DB 421 TTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 480
QY 481 AAGTGAAGTTCCTTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 540
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    481 AAGTGAAGTTCCTTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 540
DB 481 AAGTGAAGTTCCTTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 540
QY 541 CTTTTCACCTTGGGTTCAAAATTAATTAATTAATTAATTAATTAATTAATTAAT 600
    |||||
    541 CTTTTCACCTTGGGTTCAAAATTAATTAATTAATTAATTAATTAATTAATTAAT 600
DB 541 CTTTTCACCTTGGGTTCAAAATTAATTAATTAATTAATTAATTAATTAATTAAT 600
QY 601 AATTCCTCTTCAGATGATGATGATGATGATGATGATGATGATGATGATGATG 660
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    601 AATTCCTCTTCAGATGATGATGATGATGATGATGATGATGATGATGATGATG 660
DB 601 AATTCCTCTTCAGATGATGATGATGATGATGATGATGATGATGATGATGATG 660
QY 661 CAGTTTAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 720
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    661 CAGTTTAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 720
DB 661 CAGTTTAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 720
QY 721 CAGACTTTTGTACCAAGCTGATGATGATGATGATGATGATGATGATGATGATG 780
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Db 721 CAGACTTTTGTACAGCTGATGATCAACAATCTTGTTCAGAAAGTCGATACAGAA 780
Qy 781 ACTGGCACTCCCTTAATTTGATTAATAAATAATTAATACAGTATCGATATCTCATTTTC 840
Db 781 ACTGGCACTCCCTTAATTTGATTAATAAATAATTAATAATACAGTATCGATATCTCATTTTC 840
Qy 841 TTGGTTGGGAGATCAGAAAAGAGACAAAGGCTAAGCTCTTACTTGTTCGGAGTTA 900
Db 841 TTGGTTGGGAGATCAGAAAAGAGACAAAGGCTAAGCTCTTACTTGTTCGGAGTTA 900
Qy 901 GGTGAGGAGACACATATGATGAATGAATCTTAATTTGGGGTCAACCAAGATGTCTC 960
Db 901 GGTGAGGAGACACATATGATGAATGAATCTTAATTTGGGGTCAACCAAGATGTCTC 960
Qy 961 TCTCGAGGTTGGGGGGTCCCTAAGTTGATGAGCAATACCAATATATACCTAACAA 1020
Db 961 TCTCGAGGTTGGGGGGTCCCTAAGTTGATGAGCAATACCAATATATACCTAACAA 1020
Qy 1021 ACCCAATCCATGCTATACATATACATATGATCCATGATCTGTAGACTGACCCCTTCATCA 1080
Db 1021 ACCCAATCCATGCTATACATATACATATGATCCATGATCTGTAGACTGACCCCTTCATCA 1080
Qy 1081 AGAGCACCATGG 1092
Db 1081 AGAGCACCATGG 1092

RESULT 7
US-10-412-000-5
; Sequence 5, Application US/10412000
; Publication No. US20030182689A1
; GENERAL INFORMATION:
; APPLICANT: ALBERTSEN, MARC C.
; APPLICANT: FOX, TIM
; APPLICANT: HOFFMAN, GARY
; APPLICANT: TRIMMEL, MARY
; TITLE OF INVENTION: NUCLEOTIDE SEQUENCES MEDIATING MALE FERTILITY AND
; FILE REFERENCE: 1148
; CURRENT APPLICATION NUMBER: US/10/412,000
; CURRENT FILING DATE: 2003-04-11
; PRIOR APPLICATION NUMBER: US/09/670,153
; PRIOR FILING DATE: 2001-06-11
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 1092
; TYPE: DNA
; ORGANISM: Zea mays
US-10-412-000-5

Query Match 28.0%, Score 1092, DB 16, Length 1092;
Best Local Similarity 100.0%, Pred. No. 9, 2e-291;
Matches 1092; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAATTCAGAGCGAGGCGCTTGTAGAGAGAGTGTGCTGATGAGTCCGGCGAAATGAGT 60
Db 1 GAATTCAGAGCGAGGCGCTTGTAGAGAGAGTGTGCTGATGAGTCCGGCGAAATGAGT 60
Qy 61 GCGTGTGAGAGCAAGCTGAGGGGTTCCAGGGATGCGAATGCGCTATGCGACTAG 120
Db 61 GCGTGTGAGAGCAAGCTGAGGGGTTCCAGGGATGCGAATGCGCTATGCGACTAG 120
Qy 121 AGGTGAGAGCAAGGTGTGAGAGATTTGGAGGCAACCTATGCGAAGTTGTGAAGAGC 180
Db 121 AGGTGAGAGCAAGGTGTGAGAGATTTGGAGGCAACCTATGCGAAGTTGTGAAGAGC 180
Qy 181 AGCGATGAGAGATCTATTACACTTACACTGATGCGCGCAAAATTCACCTTTAG 240
Db 181 AGCGATGAGAGATCTATTACACTTACACTGATGCGCGCAAAATTCACCTTTAG 240
Qy 241 TTTGTAAGTGTCACTCTTAATTATCTTGTGTTGGGCAACTTCGATAGGCTCATGTT 300
Db 241 TTTGTAAGTGTCACTCTTAATTATCTTGTGTTGGGCAACTTCGATAGGCTCATGTT 300

Db 241 TTTGTAAGTGTCACTCTTAATTATCTTGTGTTGGGCAACTTCGATAGGCTCATGTT 300
Qy 301 AATTCATGATTTGATTAATTAATGCAAAATATCTTGTGTTGACATTAATAATG 360
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Qy 361 GGTGAGAGCGATTAATATCATTCATGAGAGCTTATCTTCATGCTCTTGAATTTGG 420
Db 361 GGTGAGAGCGATTAATATCATTCATGAGAGCTTATCTTCATGCTCTTGAATTTGG 420
Qy 421 TTTGATGATCTTCTTCAAGTGTCAAGAAATTTTCTCAGTTTGGTCCATGTAATTTTG 480
Db 421 TTTGATGATCTTCTTCAAGTGTCAAGAAATTTTCTCAGTTTGGTCCATGTAATTTTG 480
Qy 481 AAGTGAAGTCTTAAATTTCAATTAATGCTCTTCTTCTTCAAGCTGCACTGATGA 540
Db 481 AAGTGAAGTCTTAAATTTCAATTAATGCTCTTCTTCTTCAAGCTGCACTGATGA 540
Qy 541 CTTTTCATCTTGGGTTCAAAATTTGACATCAAGAAACAAATTCATCTTTGGGTTCA 600
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Qy 601 AATTCCTTTCAGAGATGATCTTTTCACTTGAACCTGTATGATGAGAAATGAGCT 660
Db 601 AATTCCTTTCAGAGATGATCTTTTCACTTGAACCTGTATGATGAGAAATGAGCT 660
Qy 661 CAGTTTAAAGAAATGATGATTAATTCATTTCAAGTCTTCTTCTGTTGGTGAATTT 720
Db 661 CAGTTTAAAGAAATGATGATTAATTCATTTCAAGTCTTCTTCTGTTGGTGAATTT 720
Qy 721 CAGACTTTTGTACAGCTGATGATCAATATCTTGTTCAGAAAGTCTGATTAACAGA 780
Db 721 CAGACTTTTGTACAGCTGATGATCAATATCTTGTTCAGAAAGTCTGATTAACAGA 780
Qy 781 ACTGGCACTCTTAATGATTAATAAAGATTAATAATACAGTATGATATCTCATTTTC 840
Db 781 ACTGGCACTCTTAATGATTAATAAAGATTAATAATACAGTATGATATCTCATTTTC 840
Qy 841 TTGGTTGGGAGATCAAAAAGAGACAAAGGCTTAAAGCTCTTCTTGGGAGTTA 900
Db 841 TTGGTTGGGAGATCAAAAAGAGACAAAGGCTTAAAGCTCTTCTTGGGAGTTA 900
Qy 901 GGTGAGGAGACACATATGATGAATGAATCTTAATTTGGGGTCAACCAAGATGTCTC 960
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Db 961 TCTCGAGGTTGGGGGGTCCCTAAGTTGATGAGCAATACCAATATATACCTAACAA 1020
Qy 1021 ACCCAATCCATGCTATACATATACATATGATCCATGATCTGTAGACTGACCCCTTCATCA 1080
Db 1021 ACCCAATCCATGCTATACATATACATATGATCCATGATCTGTAGACTGACCCCTTCATCA 1080
Qy 1081 AGAGCACCATGG 1092
Db 1081 AGAGCACCATGG 1092

RESULT 8
US-10-767-701-13826
; Sequence 13826, Application US/10767701
; Publication No. US20040172684A1
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53535)B
; CURRENT APPLICATION NUMBER: US/10/767,701
; CURRENT FILING DATE: 2004-01-29
; NUMBER OF SEQ ID NOS: 63128

SEQ ID NO 13826
LENGTH: 1898
TYPE: DNA
ORGANISM: Sorghum bicolor
FEATURES:
OTHER INFORMATION: Clone ID: SORBI-28MAY03-CLUS46299_1
US-10-767-701-13826

Query Match 27.8%; Score 1083.8; DB 19; Length 1898;
Best Local Similarity 76.1%; Pred. No. 2,4e-288;
Matches 1665; Conservative 0; Mismatches 132; Indels 392; Gaps 11;

QY 1091 GGAGGAGCTCATATCAGCGCGGAGCGCATGCGCATCTTCTCCACTACAGGCGCTCA 1150
DB 7 GGAGGAGCTCATATCAGCGCGGAGCGCATCTTCTCCACTACAGGCGCTCA 60
QY 1151 CAAGTACATGCGCGCTCTCTCTGTTGTCCTCTCATATGATCTGGTCCAGAGTGAAGCT 1210
DB 61 CAAGTACATGCGCGCTCTCTCTGTTGTCCTCTCATATGATCTGGTCCAGAGTGAAGCT 120
QY 1211 GAGGAGCAGAAAGGCCCGAGATCATGCGCATGCTGTTGCAACGGTGGAGCACTGAG 1270
DB 121 GAGGAGCAGAAAGGCCCGAGATCATGCGCGCATGCTGTTGCAACGGTGGAGCACTGAG 180
QY 1271 GAACCTACACCGGATGAGAGCTGGCTTGTGCGGTACCTGTCAACGGACAGAGCACTGAG 1330
DB 181 GAACCTACACCGGATGAGAGCTGGCTTGTGGTGTACTGTCAACGGACAGAGCACTGAG 240
QY 1331 CGTGCATGCGCGCTTCACTTCTTACACTTACATCGTGAACCGGTTGAATGTCAGCATGT 1390
DB 241 CGTGCATGCGCGCTTCACTTCTTACACTTACATCGTGAACCGGTTGAATGTCAGCATGT 300
QY 1391 CCTCAAGACTTAACTTCACTCACTTAACTCCCAAGATTAATGACTTAATCTCACTGATGTTCA 1450
DB 301 CCTCAAGACTTAACTTCACTCACTTAACTCCCAAGATTAATGACTTAATCTCACTGATGTTCA 329
QY 1451 TCTTCGGAATCAGAGCTGAAGCTGAATGATGTGCTGAAACCGCTGTAGGAATG 1510
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QY 1511 TGTACAGATCTTACATGAGCGTGTCTCTCGGTGACGGCATCTTCAACGCGAGCGAGC 1570
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QY 1571 TGTGAGGAGAGCAGAGAGACGCGCATGTTGCAATGCTTCCCAAGAACTTGAAGGATTT 1630
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DB 519 CCAAGGACGCAAAAGTTGTGAGCATG----- 544
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DB 545 ATGAGCATTTCAAACCTGAGACAGAGACTTCTTGCCGATTGAGAACTTTTACATGAG 562
QY 1811 ATGAGCGTGGAGCTCATCTGCAAGTTTGGGTTGGGGTGGAGTCCGCAACGCTGTGCGCG 1870
DB 563 ATGAGCGTGGAGCTCATCTGCAAGTTTGGGTTGGGGTGGAGTCCGCAACGCTGTGCGCG 622
QY 1871 GATCTCCCGAAGAACGCTTCCGCAAGCGCTTGCATGCGCGCAACATCATCTGTCAAGCTG 1930
DB 623 GATCTCCCGAAGAACGCTTCCGCAAGCGCTTGCATGCGCGCAACATCATCTGTCAAGCTG 682
QY 1931 CGGTTTATGAGACCGCGCTGTGCGCATCAAGAGTTCTTCCACGTGCGGTCAAGAGCGCTTC 1990
DB 683 CGGTTTATGAGACCGCGCTGTGCGCATCAAGAGTTCTTCCACGTGCGGTCAAGAGCGCTTC 742
QY 1991 CTAGCGCAGAGCATCAAGCTGTGAGCAAGTTCACTTACGCTGATCCGCGGAGAGAG 2050

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QY 2111 TTCGATTTCTTCAAGTTCACTGTCTTGGCCGCGGATGACCTGATCTGATTGATTATATTC 2170
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DB 843 CGTGTGACTTGTGAGGACAATTTAAATGGGCAATGAGCAAGATCTGTCAAGCTT 870
QY 2231 CATGAGCTAGGCGAGCGCGGCGACAGCGCGCGCTTCCGCGGAGCAAGAGCTTCCG 2290
DB 871 CATGAGCTAGGCGAGCGCGGCGACAGCGCGCGCTTCCGCGGAGCAAGAGCTTCCG 927
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QY 2411 CGCGTTGAGAGCGAGCGCGCGCGAGAGAGGCGCTGTGCTGCTCCGCGCGCGCG 2470
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DB 1162 CGACAGCGCTCGGCAAGCTGTCTTACCTCAACCGCTGCGGACAGAGAGCTCCGCTGTA 1221
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QY 2831 GGC CGGAGCGGTGATCAACGAGATGCGCGCTTCCGCAACGCGTGCCTTCAAGTTCA 2890
DB 1371 GGC CGGAGCGGTGATCAACGAGATGCGCGCTTCCGCAACGCGTGCCTTCAAGTTCA 1430
QY 2891 CGGCGTTCAAGCGCGGCGGAGAGTCTGCTGCGGCAAGGACTCCGCTGATCTGCGAGATGA 2950
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QY 2951 AGATGCGCTGCGCATCTTGTGCGCTTCTACAGCTTCCGCGTGTGAGAGGAGACCCCG 3010
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QY 3011 TGAAGTACGCAATGATACATCTCTTCATGAGCGGACAGGCTTCAAGGCTCGCGTCTTCA 3070
DB 1551 TGAAGTACGCAATGATACATCTCTTCATGAGCGGACAGGCTTCAAGGCTCGCGTCTTCA 1610
QY 3071 GGGCGGTGATGATGATGAGGATTTGGGATATCATCCCGCTTAATCTTAAAT----- 3125


```
/ APPLICANT: La Rosa, Thomas J.
/ APPLICANT: Kovalic, David K.
/ APPLICANT: Zhou, Yihua
/ APPLICANT: Cao, Yongwei
/ APPLICANT: Wu, Wei
/ APPLICANT: Boukharov, Andrey A.
/ APPLICANT: Barbazuk, Brad
/ APPLICANT: Li, Ping
/ TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated with
/ FILE REFERENCE: 38-21(53221)B
/ CURRENT APPLICATION NUMBER: US/10/437,963
/ CURRENT FILING DATE: 2003-05-14
/ NUMBER OF SEQ ID NOS: 204966
/ SEQ ID NO 51459
/ LENGTH: 330
/ TYPE: DNA
/ ORGANISM: Oryza sativa
/ FEATURE:
/ NAME/KEY: unsure
/ LOCATION: (1) - (330)
/ OTHER INFORMATION: unsure at all n locations
/ FEATURE:
/ OTHER INFORMATION: Clone ID: PAT_MRT4530_53849C.1
US-10-437-963-51459
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Query Match 5.5%; Score 214.6; DB 19; Length 330;

Best Local Similarity 81.5%; Pred. No. 2.7e-48; Matches 274; Conservative 0; Mismatches 55; Indels 7; Gaps 2;

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DB 1 CCCTTCATGAGAGAGCCCATGAGAGAACTCATATGAGCAATGCAATGAGC-----ATCATTC 54
QY 1131 TTCCCACTAGCAGGGGCTCAAGATACATGCGCTCTCTGTTGTCTCTATGAGATC 1190
DB 55 TTCCCACTAGCAGAAATCCCAAGCTCATATGCTATCTCTTGTGTCTCTATGAGATC 114
QY 1191 CTGGTCAGAGGAGGAGCCCTGAGAGAGCAAGAGGCGCGAGATCATGGCCATCGGAT 1250
DB 115 TTGGTCAGAGGAGGAGCCCTGAGAGAGCAAGAGGCGCGAGATCATGGCCATCGGAT 174
QY 1251 GCAACGATGAGAGGAGCTGAGAGAACTACACCGGATGACAGATGCTGCTGTGCGGTA 1310
DB 175 GCGACAGTGAAGAGCACTGAGAGAACTACACAGAGATGATGATGCTGCTGTGCGGTA 234
QY 1311 TCACGGACACAGACAGTACCGTTCAGATCCGTTCACTTCTTACACTAC-ATGCGCTGA 1369
DB 235 TCGAAGAGACAGACCGGTCAGATCGCTTTCACCTCTTACACTACATTTGCCGA 294
QY 1370 CCGGTCGAATGTGAGACATGCTCTCAAGACTACTT 1405
DB 295 CCGGTCGAATGTGAGACATGCTCTCAAGACTACTT 330
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RESULT 15

US-10-437-963-75572/c

/ Sequence 75572, Application US/10437963

/ Publication No. US2004012343A1

/ GENERAL INFORMATION:

/ APPLICANT: La Rosa, Thomas J.

/ APPLICANT: Kovalic, David K.

/ APPLICANT: Zhou, Yihua

/ APPLICANT: Cao, Yongwei

/ APPLICANT: Wu, Wei

/ APPLICANT: Boukharov, Andrey A.

/ APPLICANT: Barbazuk, Brad

/ APPLICANT: Li, Ping

/ TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated with

/ FILE REFERENCE: 38-21(53221)B

/ CURRENT APPLICATION NUMBER: US/10/437,963

/ CURRENT FILING DATE: 2003-05-14

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/ NUMBER OF SEQ ID NOS: 204966
/ SEQ ID NO 75572
/ LENGTH: 444
/ TYPE: DNA
/ ORGANISM: Oryza sativa
/ FEATURE:
/ OTHER INFORMATION: Clone ID: PAT_MRT4530_75649C.1
US-10-437-963-75572
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Query Match 4.6%; Score 181; DB 19; Length 444;

Best Local Similarity 86.9%; Pred. No. 6.5e-39; Matches 199; Conservative 0; Mismatches 30; Indels 0; Gaps 0;

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QY 2853 GGATGGCGGCTCCGCAAGCGCTCCGCTCAAGTTCAAGCGGCTCCAGCGGCGGCGAG 2912
DB 437 GGCGGCGGCTCCGCAAGCGCTCCGCTCAAGTTCAAGCGGCTCCAGCGGCGGCGG 378
QY 2913 GATTCGCTGGGCAAGACTCGGCGTACCTGAGATGAAGATGGCGCTGCTCTT 2972
DB 377 GATTCGCTGGGCAAGACTCGGCGTACCTGAGATGAAGATGGCGCTGCTCTT 318
QY 2973 GCGCTTCTACAGCTTCGCGCTGCTGAGAGGAGACCGGCTGCACTACCGCATATGACAT 3032
DB 317 CCGCTTCTACAGCTTCGAGACTGCTGAGAGACCAACCGCTCAAGTACCGGATGATGACAT 258
QY 3033 CCTTCATAGGAGCAAGGCTCAAGGTCGAGGCTCTTACGCGGCTGA 3081
DB 257 CCTTCATAGGCTCAAGGCTCAAGGTCGAGGCTCTTACGCGGCTGA 209
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Search completed: September 24, 2005, 19:09:27

Job time : 2375 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 24, 2005, 09:52:15 ; Search time 602 Seconds
(without alignments)
10592.310 Million cell updates/sec

Title: US-10-021-657-7

Perfect score: 3897
Sequence: 1 gattcccaagcagcgccctt.....gtctgagtaaacgacgattcc 3897

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents NA: *
1: /cgm2_6/prodata/1/ina/5A COMB. seq: *
2: /cgm2_6/prodata/1/ina/5B COMB. seq: *
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4: /cgm2_6/prodata/1/ina/5B COMB. seq: *
5: /cgm2_6/prodata/1/ina/5A COMB. seq: *
6: /cgm2_6/prodata/1/ina/5B COMB. seq: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	119.6	3.1	1626	3	US-09-158-767-14 Sequence 14, Appl
2	119.6	3.1	1626	4	US-09-713-794-14 Sequence 14, Appl
3	119.6	3.1	2181	3	US-09-158-767-10 Sequence 10, Appl
4	119.6	3.1	2181	4	US-09-713-794-10 Sequence 10, Appl
5	65.4	1.7	77536	4	US-09-410-551B-1 Sequence 1, Appl
6	65.4	1.7	77536	4	US-09-410-551B-1 Sequence 1, Appl
7	62.8	1.6	1078	3	US-09-452-239-41 Sequence 41, Appl
8	60	1.5	1822	4	US-09-502-540-8986 Sequence 8986, Ap
9	60	1.5	2943	4	US-09-502-540-3929 Sequence 3929, Ap
10	60	1.5	9125	4	US-09-902-540-959 Sequence 959, App
11	60	1.5	21285	4	US-09-902-540-1194 Sequence 1194, Ap
12	59.8	1.5	1926	3	US-09-249-585A-4 Sequence 4, Appl
13	59.8	1.5	1931	2	US-09-130-114-2 Sequence 2, Appl
14	58.6	1.5	3957	4	US-10-237-551-193 Sequence 193, Appl
15	58.6	1.5	154746	4	US-09-827-688-8 Sequence 8, Appl
16	58.6	1.5	154746	4	US-09-827-688-8 Sequence 8, Appl
17	58.2	1.5	49377	1	US-08-764-233A-1 Sequence 1, Appl
18	58	1.5	350	3	US-09-197-649-7 Sequence 7, Appl
19	57.6	1.5	528	4	US-09-902-540-7053 Sequence 7053, Ap
20	57.6	1.5	4835	4	US-09-902-540-627 Sequence 627, App
21	57.4	1.5	819	4	US-09-266-965-98 Sequence 98, Appl
22	57.4	1.5	1018	3	US-09-452-239-35 Sequence 35, Appl
23	57.4	1.5	3765	4	US-09-266-965-9 Sequence 9, Appl
24	57.4	1.5	4826	4	US-09-772-304A-1 Sequence 1, Appl
25	57.4	1.5	53500	4	US-09-266-965-76 Sequence 76, Appl
26	57.2	1.5	3794	4	US-09-192-434-1 Sequence 1, Appl
27	56.4	1.4	3382	2	US-08-682-847-1 Sequence 1, Appl

28	56	1.4	900	5	PCT-US95-04801-3 Sequence 3, Appl
29	56	1.4	2358	4	US-09-902-540-2632 Sequence 2632, Ap
30	56	1.4	17173	4	US-09-902-540-1122 Sequence 1122, Ap
31	55.4	1.4	894	4	US-09-902-540-7513 Sequence 7513, Ap
32	55.4	1.4	4845	4	US-09-902-540-730 Sequence 730, App
33	55.2	1.4	2799	3	US-09-232-279-1 Sequence 1, Appl
34	55.2	1.4	2799	4	US-10-085-519-1 Sequence 1, Appl
35	55.2	1.4	23673	3	US-09-773-816-1 Sequence 1, Appl
36	55	1.4	2721	6	5215881-2 Patent No. 5215881
37	55	1.4	2721	6	5215881-2 Patent No. 5215881
38	55	1.4	8438	1	US-07-945-283-1 Sequence 1, Appl
39	55	1.4	12173	4	US-09-902-540-1022 Sequence 1022, Ap
40	55	1.4	44377	2	US-08-804-227C-7 Sequence 7, Appl
41	55	1.4	44377	2	US-08-804-198-1 Sequence 1, Appl
42	54.6	1.4	1110	3	US-09-342-143-1 Sequence 1, Appl
43	54.6	1.4	1110	4	US-09-924-439-1 Sequence 1, Appl
44	54.4	1.4	1361	4	US-09-614-912-37 Sequence 37, Appl
45	54.4	1.4	1623	4	US-09-902-540-4832 Sequence 4832, Ap

ALIGNMENTS

RESULT 1
US-09-158-767-14

Sequence 14, Application US/09158767A

Patent No. 6180363

GENERAL INFORMATION:

APPLICANT: Batard, Yannick

APPLICANT: Durst, Francis

APPLICANT: Schalk, Michel

APPLICANT: Merck-Reichart, Daniele

TITLE OF INVENTION: RECODING OF DNA SEQUENCES PERMITTING

TITLE OF INVENTION: EXPRESSION IN YEAST AND OBTAINED TRANSFORMED YEAST

FILE REFERENCE: A32000

CURRENT APPLICATION NUMBER: US/09/158,767A

EARLIER FILING DATE: 1998-09-23

EARLIER APPLICATION NUMBER: FR 97-12094

NUMBER OF SEQ ID NOS: 20

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 14

LENGTH: 1626

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Altered sequences

US-09-158-767-14

Query Match

Best Local Similarity

Matches 219; Conservative

Score 119.6; DB 3; Length 1626;

Pred. No. 2.9e-20;

Mismatches 144; Indels 3; Gaps 1;

2691 CGCGAGACCCCAAGGGATCTTGAAGACAGCTGCGCGAGACCAAGGTGAG 2750

1149 CCGGAGACCTCAAGACAGCTGCGCGAGACCAAGGTGAG 1208

2751 GCGCGCGGATGTGACGTGACGTGACGTGACGTGACGTGACGTGACGTGAC 2810

1209 GCGCGGATGTGACGTGACGTGACGTGACGTGACGTGACGTGACGTGACGT 1268

2811 CCGGAGACCCCAAGGGATCTTGAAGACAGCTGCGCGAGACCAAGGTGAG 2867

1269 GCGCGGATGTGACGTGACGTGACGTGACGTGACGTGACGTGACGTGACGT 1328

2868 CAACGGTGCCTTCAAGTTCAGCGCGGATCTTGAAGACAGCTGCGCGAGACCA 2927

1329 GCGAGACAGCTGACAGTTCAGCGCGGATCTTGAAGACAGCTGCGCGAGACCA 1388

2928 GCGAGACAGCTGACAGTTCAGCGCGGATCTTGAAGACAGCTGCGCGAGACCA 2987

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Dd	1449	GACCGTGGCCGCCGGCCACCGCGTGAACAAGAATGTCCCTCACGCTTTTCATTAAAGG	1508
Oy	3048	CGGCTT	3053
Dd	1509	CGGCTT	1514

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RESULT 2
US-09-713-794-14
; Sequence 14, Application US/09713794
; Patent No. 678737
; GENERAL INFORMATION:
; APPLICANT: Batard, Yannick
; APPLICANT: Durst, Francis
; APPLICANT: Schalk, Michel
; APPLICANT: Werck-Reichardt, Daniele
; TITLE OF INVENTION: RECORDING OF DNA SEQUENCES PERMITTING
; TITLE OF INVENTION: EXPRESSION IN YEAST AND OBTAINED TRANSFORMED YEAST
; FILE REFERENCE: A32000
; CURRENT APPLICATION NUMBER: US/09/713,794
; CURRENT FILING DATE: 2000-11-15
; PRIOR APPLICATION NUMBER: 09/158,767
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: FR 97-12094
; PRIOR FILING DATE: 1997-09-24
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 14
; LENGTH: 1626
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION:
; US-09-713-794-14

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					Gaps 1
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Db	1149	CCCCGAGGACTCCAAAGCAGTCTGTGCGGAGGACTACCTCCCGACGGCACCCTTCGTGCC	1208		
QY	2751	GGCGCGCGCGGATGTGTGACGTACGTGCGCTTACTCGATGTGGGGGGGATGTGAGTACCACTGGGG	2810		
Db	1209	GGCGCGGCTGTGCGGTCACTACTTCACATTAATCTCGCGCGGGGCGCATGAAGGGGGTGTGGGG	1268		
QY	2811	CCCCGACGCGGCGGAGCTTCCGCGCGGAGCGGTGTGATCAACAGAGATGGCGC---GTTCCG	2867		
Db	1269	GGAGGACTGTGCTCGAGTTCCGGCGCGGAGCGATGTGTGTGTGCGGCCACGCGCACCAAGTTGGA	1328		
QY	2868	CAAGCGCTGCGCGGTTCAAGTTCACGCGGTTCCAGCGGGGCGGAGAGTCTGCTTGGCGAA	2927		
Db	1329	GCAGACACGACTCGTACCAAGTTCTGTGGCGTTTCAAGCGCGCGCGCGAGGGGTGTGCTCGGGCAA	1388		
QY	2928	GAAGTCGGCGGTACCTGACGATGAGAGATGGCGTGGCCATCTCTTGTGGCTTTACAGCTT	2987		
Db	1389	GGACTTACCTTACTCTGACGATGAGAGACATGCGCGGGAGCTGTGCTTCGCGCACCGGCTT	1448		
QY	2988	CGGCGCTGTGAGGGGCGACCGCGTGCAGTACCGCATGTATGACATCTCTTCCATGTGGCGCA	3047		
Db	1449	GACGTGGCGCGCGGGCGACCGCGGTGTGAGCAGAAAGATGTGCGTCAAGCGCTTTCATGAAGGG	1508		
QY	3048	CGGCGCT 3053			
Db	1509	CGGCGT 1514			

```

? Patent No 6180363
? -----
? GENERAL INFORMATION:
?
? APPLICANT: Batard, Yannick
? APPLICANT: Duret, Francis
? APPLICANT: Schalk, Michel
? APPLICANT: Werck-Reichardt, Daniele
?
? TITLE OF INVENTION: RECODING OF DNA SEQUENCES PERMITTING
? TITLE OF INVENTION: EXPRESSION IN YEAST AND OBTAINED TRANSFORMED YEAST
?
? FILE REFERENCE: A32000
?
? CURRENT APPLICATION NUMBER: US/09/158,767A
?
? CURRENT FILING DATE: 1998-09-23
?
? EARLIER APPLICATION NUMBER: FR 97-12094
?
? EARLIER FILING DATE: 1997-09-24
?
? NUMBER OF SEQ ID NOS: 20
?
? SOFTWARE: PaatsBG for Windows Version 3.0
?
? SEQ ID NO 10
?
? LENGTH: 2181
?
? TYPE: DNA
?
? ORGANISM: Triticum aestivum
?
? US-09-158-767-10

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Query Match	3.14; Score 119.6; DB 3; Length 2181;
Best Local Similarity	59.84; Pred. No. 3.5e-20;
Matches 219; Conservative	0; Mismatches 144; Indels 3; Gaps 1
Qy 2691	CGCGCAGAGCCCAAGGGGATCTTGAGAGCAGCGTGTGCGGACGGGACGAAAGTGA 2750
Db 1260	CCCCGAGGACTCCAAGCAGCGTGTGCGGAGCAGTACTCTCCCGACGGCACCCTGTGTC 1311
Qy 2751	GGCCGGCGGGATGGTGAAGTACGTGCGCTTACTCGATGGGGCGGATGAGTACACTGGGG 2811
Db 1320	GGCCGGGTGTGTGGTACCTACTCATATATCTGGCGGGGGCGATGAAAGGGGGTGTGGGG 1375
Qy 2811	CCCCGACGGCGGAGAGCTTCCGGCGCGAGCGGTGATCAACGAGATGAGCGC---GTTCG 2867
Db 1380	GGAGAGCTGCTCGAGTTCCGGCCCGGACGATGCTGTGCGGCCGACGGCACCMACTTGA 1433
Qy 2868	CAACGCGCTGCGCGTTCAAATTACGCGCGCTTCAAGCGGGGCGGAGATGTGCTGGGCA 2927
Db 1440	GCACACAGACTGTATCAAGATTGTGGCGCTTCAACGCGCGGCGCGAGGGTGTGCTGGGCA 1495
Qy 2928	GGACTCGGCGATACCTGAGATGAAGATGCGGCTGGCCATTCCTTTGGGCTTCTACAGCTT 2987
Db 1500	GGACTTACCTTACCTGCGAGATGAAGAACATGCGCGGAGCGTGTGCTGTCCGGCACCGCTT 1555
Qy 2988	CCGGCTGTGAGGGGGCAACCCGATGACGTACCGCATGTATGACATCTCTCCATGGCGCA 3047
Db 1560	GACCGTGGCGCGGGGCCACCGCGGTGAGCAGAAAGATGTCGCTTCAACGCTTTCATGAAGG 1611
Qy 3048	CGGCGCT 3053
Db 1620	CGGCGCT 1625

RESULT 3
US-09-158-767-10
; Sequence 10, Application US/09158767A

```

RESULT 4
US-09-713-794-10
: Sequence 10, Application US/09713794
: Patent No. 6787337
: GENERAL INFORMATION:
: APPLICANT: Batard, Yannick
: APPLICANT: Durst, Francis
: APPLICANT: Schalk, Michel
: APPLICANT: Merck-Reichardt, Daniele
: TITLE OF INVENTION: RECODING OF DNA SEQUENCES PERMITTING
: TITLE OF INVENTION: EXPRESSION IN YEAST AND OBTAINED TRANSFORMED YEAST
: FILE REFERENCE: A22000
: CURRENT APPLICATION NUMBER: US/09/713,794
: CURRENT FILING DATE: 2000-11-15
: PRIOR APPLICATION NUMBER: 09/158,767
: PRIOR FILING DATE: 1998-09-23
: PRIOR APPLICATION NUMBER: FR 97-12094
: PRIOR FILING DATE: 1997-09-24
: NUMBER OF SEQ ID NOS: 20

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SOFTWARE: FaetsBQ for Windows Version 3.0
 SEQ ID NO 10
 LENGTH: 2181
 TYPE: DNA
 ORGANISM: Trilicium aestivum
 US-09-713-794-10

Query Match 3.1%; Score 119.6; DB 4; Length 2181;
 Best Local Similarity 59.8%; Pred. No. 3.5e-20;
 Matches 219; Conservative 0; Mismatches 144; Indels 3; Gaps 1;

QY 2691 CCGCAGAGACCCCAAGGGGATCTTGAAGAGACGATGCTGCGGACCGGACGAAAGTGA 2750
 DB 1260 CCCCAGAGACTCCAGAGACGTCGTGCGGAGACTACTCCCGAGCGGACCTTGTGCGC 1319
 QY 2751 GGGCGCGGAGATGTGACGTAAGTCCCTTACTGATGCGGCGGATGAGTGAACATGCGG 2810
 DB 1320 GGGCGGATGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1379
 QY 2811 CCGCAGCGCGGAGCTTCCGCGCGGAGCGGATGATCAAGAGATGCGGCGGCTTCCG 2867
 DB 1380 GAGAGACTGCTGAGTTCGCGCGCGGAGCGATGCTGCTGCGCGGACGAAAGTTCGA 1439
 QY 2868 CAAAGCGCTGCGCTTCAAGTTCAAGCGCTTCAAGCGCGGCGCGGAGATGCTGCGGCAA 2927
 DB 1440 GAGAGAGACTGCTGAGTTCGCGCGCGGAGCGATGCTGCTGCGCGGACGAAAGTTCGA 1499
 QY 2928 GAGACTGCGCTTCAAGTGAAGATGAGCGCGCTGCGGCGGCTTCCGCTTCAAGCTT 2987
 DB 1500 GAGACTGCGCTTCAAGTGAAGATGAGCGCGCTGCGGCGGCTTCCGCTTCAAGCTT 1559
 QY 2988 CCGCGCTGCTGAGAGCGGCGCGGAGCGGATGAGCGGCGGCGGCGGCGGCGGCGGCGG 3047
 DB 1560 GACCGTGGCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1619
 QY 3048 CCGCGCT 3053
 DB 1620 CCGGCT 1625

RESULT 5
 US-09-410-551B-1
 Sequence 1, Application US/09410551B
 Patent No. 6503737

GENERAL INFORMATION:
 APPLICANT: KOSAN BIOSCIENCES, Inc.
 APPLICANT: REEVES, CHRISTOPHER
 APPLICANT: CHU, DANIEL
 APPLICANT: KHOSLA, CHAITAN
 APPLICANT: SANTI, DANIEL
 TITLE OF INVENTION: POLYKETIDE SYNTHASE ENZYMES AND RECOMBINANT DNA
 FILE REFERENCE: 30062-20026.00
 CURRENT APPLICATION NUMBER: US/09/410,551B
 PRIOR APPLICATION NUMBER: US 60/139,650
 PRIOR FILING DATE: 1999-06-17
 PRIOR APPLICATION NUMBER: US 60/123,810
 PRIOR FILING DATE: 1999-03-11
 PRIOR APPLICATION NUMBER: US 60/102,748
 PRIOR FILING DATE: 1998-10-02
 NUMBER OF SEQ ID NOS: 72
 SOFTWARE: FaetsBQ for Windows Version 4.0
 SEQ ID NO 1
 LENGTH: 77536
 TYPE: DNA
 ORGANISM: Streptomyces hygroscopicus
 FEATURES:
 NAME/KEY: CDS
 LOCATION: (52275) ... (71465)
 US-09-410-551B-1

Query Match 1.7%; Score 65.4; DB 4; Length 77536;
 Best Local Similarity 51.9%; Pred. No. 3e-05;
 Matches 175; Conservative 0; Mismatches 156; Indels 6; Gaps 1;

QY 2232 ATCGAGCTAGGCGGAGCGCGGCGGAGCGGCGGCTTGGGAGGAGCAAGAGCTCCG 2291
 DB 56223 ACCGGGCGCGGCGGCTGAGCAACCTGTCCCGGAGACCGGCGGTGTCCGCTGACCCG 56282
 QY 2292 GACGTGTGTCTCACTTGTGATGCGCGGCGGAGCAAGAGCGGAGCGGCTGTG 2351
 DB 56283 GGCATGCGCGCGGCGGCGGCTGACCGGCGGCGGCTGTGCGGCGGAGTCCCGAGCGGCTG 56342
 QY 2352 TTGAGCGCATGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 2411
 DB 56343 AGCTTACCAACGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 56402
 QY 2412 GCGTTGAGGCGGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 2471
 DB 56403 GACCTGCGGCACTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 56462
 QY 2472 GACGCGGAGCAAGAGCGGCTTCCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 2531
 DB 56463 GGCATGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 56516
 QY 2532 GACAGCTGCGGAGAGCTGCTTACCTCCAGCGGCTGCG 2568
 DB 56517 GCGATGACCGGCAAGAGCAAGCTTGTGCGGCGGCGGCGG 56553

RESULT 6
 US-09-940-316B-1
 Sequence 1, Application US/0940316B
 Patent No. 6759536

GENERAL INFORMATION:
 APPLICANT: KOSAN BIOSCIENCES, Inc.
 APPLICANT: REEVES, CHRISTOPHER
 APPLICANT: CHU, DANIEL
 APPLICANT: KHOSLA, CHAITAN
 APPLICANT: SANTI, DANIEL
 TITLE OF INVENTION: POLYKETIDES ENCODING THE FBA GENE OF THE PK-520 POLYKETIDE SYNT
 FILE REFERENCE: 30062-20026.11
 CURRENT APPLICATION NUMBER: US/09/940,316B
 PRIOR APPLICATION NUMBER: 2001-08-27
 PRIOR FILING DATE: 1999-10-01
 PRIOR APPLICATION NUMBER: US 60/139,650
 PRIOR FILING DATE: 1999-06-17
 PRIOR APPLICATION NUMBER: US 60/123,810
 PRIOR FILING DATE: 1999-03-11
 PRIOR APPLICATION NUMBER: US 60/102,748
 PRIOR FILING DATE: 1998-10-02
 NUMBER OF SEQ ID NOS: 72
 SOFTWARE: FaetsBQ for Windows Version 4.0
 SEQ ID NO 1
 LENGTH: 77536
 TYPE: DNA
 ORGANISM: Streptomyces hygroscopicus
 FEATURES:
 NAME/KEY: CDS
 LOCATION: (52275) ... (71465)
 US-09-940-316B-1

Query Match 1.7%; Score 65.4; DB 4; Length 77536;
 Best Local Similarity 51.9%; Pred. No. 3e-05;
 Matches 175; Conservative 0; Mismatches 156; Indels 6; Gaps 1;

QY 2232 ATCGAGCTAGGCGGAGCGGCGGAGCGGCGGCTTGGGAGGAGCAAGAGCTCCG 2291
 DB 56223 ACCGGGCGCGGCGGCTGAGCAACCTGTCCCGGAGACCGGCGGTGTCCGCTGACCCG 56282
 QY 2292 GACGTGTGTCTCACTTGTGATGCGCGGCGGAGCAAGAGCGGAGCGGCTGTG 2351
 DB 56283 GGCATGCGCGCGGCGGCGGCTGACCGGCGGCGGCTGTGCGGCGGAGTCCCGAGCGGCTG 56342
 QY 2352 TTGAGCGCATGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 2411
 DB 56343 AGCTTACCAACGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 56402
 QY 2412 GCGTTGAGGCGGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 2471
 DB 56403 GACCTGCGGCACTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 56462
 QY 2472 GACGCGGAGCAAGAGCGGCTTCCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 2531
 DB 56463 GGCATGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 56516
 QY 2532 GACAGCTGCGGAGAGCTGCTTACCTCCAGCGGCTGCG 2568
 DB 56517 GCGATGACCGGCAAGAGCAAGCTTGTGCGGCGGCGGCGG 56553

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Db      56283 GGCATGCGCCGACGCGCCGCTCAACCGACCGCGCTGCGCCGCGATCCCGACGCGCTGG 56342
Qy      2352 TTCACGCAATGCGCCATGTCCTCCACCCCGACGTCGCGGACGAGAGTGGCCGCGACGCTGTC 2411
Db      56343 AGCTTCACCAACGCGCGCGCTGCTCCGATCGTGTTCGACCGCGGTGTACCGCCCTGTGTC 56402
Qy      2412 GCGTTCAGAGCGGAGCGCGCGCGACGAGAGGCGTGGCGCTGCTGCTGCGCGCGCGCT 2471
Db      56403 GACCTTCGACACTGCGCGCGCGCGGAGAGTCTGCTGTCACCGCGCGCACCGCGCGTGTTC 56462
Qy      2472 GACGCGGACGACAAAGCGCTTCGCGCGCGCGGTGGCGCGACGTTGCGGCGCTCTCACTAC 2531
Db      56463 GCGATGCGCGCGCGACAGATCGCGCGCGCACCTGG-----GCGCGAGCTCTACGCGCAC 56516
Qy      2532 GACAGCTTCGCGGACGCTGCTCACTCCACGCGCTGG 2568
Db      56517 GCGAGTACCGGCAAGACGACGTCCTGCGCGCGCGCG 56553
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RESULT 7
US-09-452-239-41
Sequence 41, Application US/09452239

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/ Patent No. 6465229
/ GENERAL INFORMATION:
/ APPLICANT: Rafaleki, Antoni J.
/ APPLICANT: Fader, Gary M.
/ APPLICANT: Cahoon, Rebecca E.
/ TITLE OF INVENTION: Plant Cafeoyl-CoA O-Methyltransferase
/ FILE REFERENCE: B1284 US NA
/ CURRENT APPLICATION NUMBER: US/09/452,239
/ EARLIER FILING DATE: 1999-12-01
/ EARLIER APPLICATION NUMBER: 60/110,594
/ EARLIER FILING DATE: 1998-December-02
/ NUMBER OF SEQ ID NOS: 50
/ SOFTWARE: Microsoft Office 97
/ SEQ ID NO 41
/ LENGTH: 1078
/ TYPE: DNA
/ ORGANISM: Trilicium aestivum
US-09-452-239-41
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Query Match 1.6%; Score 62.8; DB 3; Length 1078;
Best Local Similarity 48.1%; Pred. No. 1.1e-05;
Matches 178; Conservative 0; Mismatches 192; Indels 0; Gaps 0;

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Qy      2252 CGACGACGCGCGCGCTTCGCGGAGACGACGACCTTCGCGACGTCGTCTCACTTCGT 2311
Db      423 CGGACCGCGCTGCGCATCCCGACGACGACCATCTTGGCCATGACATCAACCGCA 482
Qy      2312 GATCGCGCGCGGACGACGACGCGACGACGCTGTGTGTTCACGCACTGCGCATGTC 2371
Db      483 GAACTACGAGCTGGGCTGCGCTGCTGACGAGAGCGCGCTGGCGCAAGATCACTT 542
Qy      2372 CCAACCGGACGTCGCGGAGAGCTGCGCGCGACGCTGTGCGCTTCGAGCGGAGCGCG 2431
Db      543 CGCGAGGCGCGCGCGCTGCGCGCTGCGCGCTGCGCGCTGCGAGAGAGAGGCGCAACCA 602
Qy      2432 GCGCGAGAGGCGCTGCGCGCTGCGCGCTGCGCGCGCGCGCGCGCGCGCGCGCGCTT 2491
Db      603 CACTTCGACTTGTCTTCTGTGACGCGCGACGAGACACTCACTCACTCAACGAGCG 662
Qy      2492 CGCGCGCGCGCGCGCGCTTCGCGCGCGCTCTCACTACGACGCGCTCGCGCAAGCTGAT 2551
Db      663 CTCGACGAGAGCTGCTCAAGCTCGCGCGCGCTCTCTGCGCTACGACGAGCAACGCTGGA 722
Qy      2552 CTACCTTCACGCGCTGCGTCAACGAGAGCTCGCGCTGTACCCCGCGCTTCAGGTGAG 2611
Db      723 CTCGCGTGTGCTCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCTT 782
Qy      2612 CGCGCGCGGAC 2621
Db      783 GGTCTCTGAC 792
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RESULT 8
US-09-902-540-8986
Sequence 8986, Application US/09902540

```
/ Patent No. 6833447
/ GENERAL INFORMATION:
/ APPLICANT: Goldman, Barry S.
/ APPLICANT: Hinkle, Gregory J.
/ APPLICANT: Slater, Steven C.
/ APPLICANT: Wiegand, Roger C.
/ TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
/ FILE REFERENCE: 38-10(15849)B
/ CURRENT APPLICATION NUMBER: US/09/902,540
/ PRIOR FILING DATE: 2001-07-10
/ PRIOR APPLICATION NUMBER: 60/217,883
/ PRIOR FILING DATE: 2000-07-10
/ NUMBER OF SEQ ID NOS: 16825
/ SEQ ID NO 8986
/ LENGTH: 1822
/ TYPE: DNA
/ ORGANISM: Myxococcus xanthus
US-09-902-540-8986
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Query Match 1.5%; Score 60; DB 4; Length 1822;

Best Local Similarity 47.2%; Pred. No. 7.7e-05;
Matches 183; Conservative 0; Mismatches 205; Indels 0; Gaps 0;

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Qy      2235 GAGCTAGCGAGCGCGCGCGCGCGCGCGCTTCGCGGACGACGACGCTCCGCGAC 2294
Db      1112 GAGGCGCGGACGCGCGCGCGCTGCGCGCTGTGAGCTTCGAGCGCTTCGACGAGCATGGA 1171
Qy      2295 GTGAGTCACTTCGTCGTCGTCGCGCGCGGACGACGCGCGCGCTGTCGTCGTC 2354
Db      1172 GAGGCGCTCAACGATGTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1231
Qy      2355 AGCAGATGCGCATGTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 2414
Db      1232 CCTCAAGGAGATGTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1291
Qy      2415 TTCAGGCGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 2474
Db      1292 CTGAGCGCGCTCTCAACGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1351
Qy      2475 GCGGACGACGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 2534
Db      1352 ACCGCGCGGACGCGCGCTTCGACGAGAGTCAAGCCGCGCGCGCGCGCGCGCGCG 1411
Qy      2595 GCGCTTCCTCAAGTGAAGCGCGCGCGCA 2622
Db      1472 CGCGAGCTGCGCGGTATTAAGCGCTTACA 1499
```

RESULT 9
US-09-902-540-3929

```
/ Sequence 3929, Application US/09902540
/ Patent No. 6833447
/ GENERAL INFORMATION:
/ APPLICANT: Goldman, Barry S.
/ APPLICANT: Hinkle, Gregory J.
/ APPLICANT: Slater, Steven C.
/ APPLICANT: Wiegand, Roger C.
/ TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
/ FILE REFERENCE: 38-10(15849)B
/ CURRENT APPLICATION NUMBER: US/09/902,540
/ PRIOR FILING DATE: 2001-07-10
/ PRIOR APPLICATION NUMBER: 60/217,883
/ PRIOR FILING DATE: 2000-07-10
/ NUMBER OF SEQ ID NOS: 16825
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SEQ ID NO 3929
LENGTH: 2943
TYPE: DNA
ORGANISM: Myxococcus xanthus
US-09-902-540-3929

Query Match 1.5%; Score 60; DB 4; Length 2943;
Best Local Similarity 43.3%; Pred. No. 0.0001;
Matches 330; Conservative 0; Mismatches 430; Indels 2; Gaps 1;

QY 2244 GAGCGCGGACGACGCGCGCGCTTCGGGACGACGACGCTCCGGGACGCTGCTC 2303
|||
DB 1597 GAGGTGGCGCGGCGCGCGCGCGCTTCGAGTTCGCGGACGCTGCTGCTGCTGCTG 1656
|||
QY 2304 AACTTGATGCTGCGCGCGCGGACGACGCGCGCGCTTCGAGTTCGCGGACGCTG 2263
|||
DB 1657 CTTGAGCGCGCGCGCGCGCGCGCTTCGAGTTCGCGGACGCTGCTGCTGCTGCTG 1716
|||
QY 2364 GCGATGTCGCGCGCGCGCGCGCGCTTCGAGTTCGCGGACGCTGCTGCTGCTGCTG 2423
|||
DB 1717 CATCGGTGAGATTCAGCTTCGACCGCGCGCGCGCGCTGCTGCTGCTGCTGCTG 1776
|||
QY 2424 GAGCGCGCGCGCGCGCGCGCGCTTCGAGTTCGCGGACGCTGCTGCTGCTGCTGCTG 2483
|||
DB 1777 CTGCTGCGCGCGCGCGCGCGCGCTTCGAGTTCGCGGACGCTGCTGCTGCTGCTG 1836
|||
QY 2484 AAGCGCTTCGCGCGCGCGCGCGCGCTTCGAGTTCGCGGACGCTGCTGCTGCTGCTG 2543
|||
DB 1837 GAGGAGGTGAGCGCGCGCGCGCGCGCTTCGAGTTCGCGGACGCTGCTGCTGCTGCTG 1896
|||
QY 2544 AAGCTGATCTACCTCCAGCGCTTCGAGTTCGCGGACGCTGCTGCTGCTGCTGCTG 2603
|||
DB 1897 TACGCGGAGAGATTCAGCTTCGACCGCGCGCGCGCGCTGCTGCTGCTGCTGCTG 1956
|||
QY 2604 CAGGTGAGCGCGCGCGCGCGCGCTTCGAGTTCGCGGACGCTGCTGCTGCTGCTGCTG 2661
|||
DB 1957 GACCGCGCTTCGAGTTCGAGTTCGCGGACGCTGCTGCTGCTGCTGCTGCTGCTG 2016
|||
QY 2662 CCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2721
|||
DB 2017 GCGGAGGAGCGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATG 2076
|||
QY 2722 GACGTGCTGCGCGCGCGCGCGCGCTTCGAGTTCGCGGACGCTGCTGCTGCTGCTGCTG 2781
|||
DB 2077 TCCGCGGTGAGGATGAGTTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2136
|||
QY 2782 TCGATGAGGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATG 2841
|||
DB 2137 ACGGTGACGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATG 2196
|||
QY 2842 TCGATGAGGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATG 2901
|||
DB 2197 GCGTTCAGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATG 2256
|||
QY 2902 GCGGCGCGGAGATGCTGCTGCGGACGAGTTCGCGGACGCTGCGGACGCTGCGGACGCTG 2961
|||
DB 2257 GACGTGATGAGGACGCGACGCGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2316
|||
QY 2962 GCCATCCTCTTGGCTTCTTCAAGCTTCGCGGACGCTGCGGACGCTGCGGACGCTG 3003
|||
DB 2317 GAGGAGTGGAGTTCCTGCGGACGCGGACGCGGCTGCTGCTGCTGCTGCTGCTGCTG 2358
|||

RESULT 10
US-09-902-540-959/c
Sequence 959, Application US/09902540
Patent No. 6833447

GENERAL INFORMATION:
APPLICANT: Goldman, Barry S.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Wiegand, Roger C.
TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof

FILE REFERENCE: 38-10(15849)B
CURRENT APPLICATION NUMBER: US/09/902,540
CURRENT FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: 60/217,883
PRIOR FILING DATE: 2000-07-10
NUMBER OF SEQ ID NOS: 16825
SEQ ID NO 959
LENGTH: 9125
TYPE: DNA
ORGANISM: Myxococcus xanthus
US-09-902-540-959

Query Match 1.5%; Score 60; DB 4; Length 9125;
Best Local Similarity 47.2%; Pred. No. 0.0002;
Matches 183; Conservative 0; Mismatches 205; Indels 0; Gaps 0;

QY 2235 GAGTGAAGGCGCGCGCGCGCGCTTCGGGACGACGACGCTCCGGGACGCTGCTC 2294
|||
DB 3957 GAGCGCGGAGCGCGCGCGCGCGCTTCGAGTTCGCGGACGCTGCTGCTGCTGCTGCTG 3898
|||
QY 2295 GTGCTGCTCACTTCGATTCGCGCGCGGACGACGCGCGCGCTTCGAGTTCGCGGACG 2354
|||
DB 3897 GAGGCGGTCAACGATGCTGCGCGCGCGCGCTTCGAGTTCGCGGACGCTGCTGCTGCTG 3838
|||
QY 2355 AGCGATGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2414
|||
DB 3837 CCTCAAGGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3778
|||
QY 2415 TTGAGGCGGAGCGCGCGCGCGCGCTTCGAGTTCGCGGACGCTGCTGCTGCTGCTGCTG 2474
|||
DB 3777 CTGAGCGCGGTCTCACTGCTGCGCGCGCGCGCTTCGAGTTCGCGGACGCTGCTGCTGCTG 3718
|||
QY 2475 GCGGACGACGAGGCTTCGCGCGCGCGCGCGCTTCGAGTTCGCGGACGCTGCTGCTGCTG 2534
|||
DB 3717 ACCGCGGCGGAGGCTTCGAGTTCGAGTTCGCGGACGCTGCTGCTGCTGCTGCTGCTG 3658
|||
QY 2535 AGCTGCGGAGGCTTCGATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTCG 2594
|||
DB 3657 GCGGAGGCTGAGTTCGATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTCG 3598
|||
QY 2595 GCGGTCTTCAGTTCGAGGCG 2622
|||
DB 3597 CCGGAGCTGCGGTGATTCAGCGCTTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 3570
|||

RESULT 11
US-09-902-540-1194
Sequence 1194, Application US/09902540
Patent No. 6833447

GENERAL INFORMATION:
APPLICANT: Goldman, Barry S.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Wiegand, Roger C.
TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
FILE REFERENCE: 38-10(15849)B
CURRENT APPLICATION NUMBER: US/09/902,540
CURRENT FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: 60/217,883
PRIOR FILING DATE: 2000-07-10
NUMBER OF SEQ ID NOS: 16825
SEQ ID NO 1194
LENGTH: 21295
TYPE: DNA
ORGANISM: Myxococcus xanthus
US-09-902-540-1194

Query Match 1.5%; Score 60; DB 4; Length 21295;
Best Local Similarity 43.3%; Pred. No. 0.00034;
Matches 330; Conservative 0; Mismatches 430; Indels 2; Gaps 1;

QY 2244 GAGCGCGGACGACGCGCGCGCTTCGGGACGACGACGCTCCGGGACGCTGCTC 2303
|||

```
Db 2375 GAGGTGGGCGGCGAGGGGCGCACTTTCAGTTGCGCCACCACTGTGGCACTACGACTG 2434
QY 2304 AACTTGTGATGCGCGGGGGGGGCAAGACGCGTGTCTGTTCACGCACTG 2363
Db 2435 CCTTGAAGCCCGGCGCGGTGGAGCAGCGCATTTGGCGGTGACCGCATGGCGCAGAGC 2494
QY 2364 GCCATGTCCACCCCGGACGTGGCGGAGAAAGCTGCGCGCAGACTGTGCGGTTTCAAGGCG 2423
Db 2495 CATCGGTGGAGATTACGCTTTTCAACCGCGGGGACGCTGGCCTCCGACGTGCTGATG 2554
QY 2424 GAGCGCGCGCGAGAGAGGGCGTGGCGCTGTGCTGCTGCGCGGCGGCTGACGCGCAAGC 2483
Db 2555 CTGCTGCGGACCGCGTGGCGGTCTTTCGCGGAGACCGGTGGCGGCTGAGCGGCTGTG 2614
QY 2484 AAGGCGTTGGCGCGCGCGGTGGCGGAGTTTCGCGGGGCTCTCACTAACGACGCGTGGC 2543
Db 2615 GAAAGAGTGGAGGCGCGGCTGGCGGAGCTGGCGCTGATGCGCGCAAGGCGCCCATGGCC 2674
QY 2544 AAGCTGATCTACTTCCACGCTTGCCTTACCGGAGACGCTCGGCTGTACCCCGCTGCTCCT 2603
Db 2675 TACGCGCAGAGAGCTGAAGGCGCGCGTGGAGGCGCGCGCGCCAGGTTGAAGCGCGCTAT 2734
QY 2604 CAGGTAGCGCGCGCCCAAC- -GCACTTCGGTCCAGAGCAAGCAATGCAATGAGTGA 2661
Db 2735 GACCCGCTCTGTGACGTGGCGCAGCTTTCAGCGCGCGGTGGAGCGCTGTGAAGCGC 2794
QY 2662 CTGGAATGCAATGCAATGCAATGCACTTGGCGCGCGCGGACCCCAAGGGAGATCTGTGAG 2721
Db 2795 GCCCAGAGAGCGCATGGGCGATCGAGCGGACGAGAGAGAGACAGGACGCGAGCGGAGGCG 2854
QY 2722 GACGTGCTGCGGACGAGAGAGAGTGAAGGCGCGGAGTGTGACGTACGTGCGCTTAC 2781
Db 2855 TCGGGGTTGAGATGAGCTGTGGGCGATGCGCGGAGCCTTGAAGAGCGGCTGTGAGAG 2914
QY 2782 TCGATGGGCGGATGAGATGACACTGGGCGCCGAGCGCGGAGCTTTCGGCGGAGCGG 2841
Db 2915 ACAGTACGAGAGCTGGCGCGCGCGGTGGCATGGGCTGTGACCAAGCAGCAGGTGGAG 2974
QY 2842 TGGATCAAGAGATGGCGGCTTCGGAACGCGTTCGCTTCAAGTTCAAGCGGCTTCAAG 2901
Db 2975 GCGTTCAAGTGGCTTTCAGTTTGGCGCAGCGCTGAGAGTGGACGAGCTGCGGGCAGTC 3034
QY 2902 GCGGGGCGGAGATCTGCTGGGCAAGACTCGGCGTACTTGCAGATGAAGATGGCGCTG 2961
Db 3035 GACGTATGAGAGACGAGCAGCAGCTGGGACCTTCTGGGCGGACACCGCGGTGGAGGCG 3094
QY 2962 GCCATCTCTTGGCGCTTTCAGAGCTTCCGCGTGGCTGGAGGCG 3003
Db 3095 GAGGAGTTGAGATTCGCGCACCGGACACCGCGTGGTGGAG 3136

RESULT 12
US-09-249-585A-4/c
; Sequence 4, Application US/09249585A
; Patent No. 6417002
; GENERAL INFORMATION:
; APPLICANT: Horlick, Robert
; TITLE OF INVENTION: METHOD FOR MAINTENANCE AND SELECTION OF EPISOMES
; FILE REFERENCE: 0867/0D905
; CURRENT APPLICATION NUMBER: US/09/249,585A
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
; LENGTH: 1926
; TYPE: DNA
; ORGANISM: Epstein Barr Virus
; NAME/KEY: m1ac feature
; LOCATION: (1)..(1926)
; OTHER INFORMATION: template strand of EBNA-1 DNA
US-09-249-585A-4
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Query Match 1.5%; Score 59.8; DB 3; Length 1926;
Best Local Similarity 43.9%; Pred. No. 8.9e-05;
Matches 306; Conservative 0; Mismatches 387; Indels 4; Gaps 1;

QY 2241 GCGAGGCGCGGACGACGCGCGCGCTTTCGGGAGCAGACAGAGAGCTTCCGGGAGCTGTG 2300
Db 952 GACGGGAGAGAGAGAGAGAGCGGGAGAGACGGGGAGAGCAGAGAGCGGGAGAGCGGGAG 893
QY 2301 CTCACCTTGTGATGCGCGGGGCGGACAGACGCGGAGACGACGCTGTGCTTCAAGCAGC 2360
Db 892 GACAGAGACGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 833
QY 2361 ATGAGCATGTCCACCGGACGTGGCGGAGAGCTGCGCGGAGAGAGAGAGAGAGAGAGAG 2420
Db 832 GGGAGAGACGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 773
QY 2421 GCGGAGCGCGCGCGGAGAGAGGCGTTCGCGCTGTGCTTGTGCGCGGCGGCTGAGCGC 2480
Db 772 GGGGAGAGACGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 713
QY 2481 GACAGGCGCTTTCGCGCGCGGTGGCGGAGTTTCGCGGGGCTCTCACTAACGACGCTC 2540
Db 712 GACAGAGACGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 653
QY 2541 GGCAGAGCTGTACTTCCACGCTGCGTCAACGAGAGAGCTTCGCGCTGTACCCCGCTC 2600
Db 652 GGGAGAGACGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 593
QY 2601 CTTCAAGTGAAGCGCGCCGACAGCGGACCTTCGGTTCAGAGAGCAGCATGCAATGAGTGG 2660
Db 592 GAGGACGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 533
QY 2661 ACTGAATGCAATGCAATGCAATGCACTTGGCGCGCGGAGAGAGAGAGAGAGAGAGAG 2720
Db 532 ----GACAGAGAGCGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 477
QY 2721 CGAGCTGTGCTCGGACGCGGACGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2780
Db 476 CGAGGACGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 417
QY 2781 CTGATGGGCGGATGAGATGACACTGGGCGCCCGACGCGCGAGCTTTCGGCGGAGCG 2840
Db 416 CGGGAGAGAGCGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 357
QY 2841 GTGATCAACGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2900
Db 356 GAGCGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 297
QY 2901 GCGGGGCGGAGATCTGCTGGGCAAGGACTCGGCG 2937
Db 296 GAGCGGGAGAGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 260

RESULT 13
US-09-130-114-2/c
; Sequence 2, Application US/09130114
; Patent No. 5976807
; GENERAL INFORMATION:
; APPLICANT: Horlick, Robert A.
; APPLICANT: Damaj, Bassem B.
; APPLICANT: Robbins, Alan K.
; TITLE OF INVENTION: Eukaryotic Cells Stably Expressing Genes
; TITLE OF INVENTION: From Multiple Transfected Episomes
; FILE REFERENCE: 0867/1D90JUS1
; CURRENT APPLICATION NUMBER: US/09/130,114
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 1931
; TYPE: DNA
; ORGANISM: EBNA
US-09-130-114-2
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Query Match 1.5%; Score 59.8; DB 2; Length 1931;
Best Local Similarity 43.9%; Pred. No. 9e-05;
Matches 306; Conservative 0; Mismatches 387; Indels 4; Gaps 1;

QY 2241 GCGGAGCGCCGCGACGACGCGCGCGCTTCCGGGAGCAGCAAGAGCTTCCGGGAGCGTGTG 2300
DB 952 GACCGGAGGAGGACGAGGACGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 893
QY 2301 CTCAACTTGTGATCGCGCGCGGAGACGACGCGGACGACGCTGTGTGTTCACGCGAC 2360
DB 892 GACGAGGACGCGGAGGAGACGCGGAGAGACGAGGACGCGGAGGAGCGGAGGAGAGAGAG 833
QY 2361 ATGGCCATGTCCACCGCGGACGTGCGCGGAGAGAGTCTGCGCGCGGAGCTGTGCGTTCGAG 2420
DB 832 GGGGAGGACGCGGAGGAG 773
QY 2421 GCGGAGCGCGCGCGCGGAGAGAGGCGTGTGCGCTGTGCGCGCGCGCGCTGACGCGGAC 2480
DB 772 GGGGAGGACGAGGACGCGGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 713
QY 2481 GACAGGCGTTCGCGCGCGCGCGCGGAGAGAGTTCGCGCGCGCTCTCACTTACAGAGCTTC 2540
DB 712 GACGAGGACGCGGAGGAG 653
QY 2541 GCGGAGCTGTGTCTACCTCCACGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2600
DB 652 GGGGAGGACGAGGACGCGGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 593
QY 2601 CCTCAGGTGAGCGCGCGCGCGCGCGAGCTTCCGGTCCAGAGCAGAGATCAGTGTGTGTG 2660
DB 592 GAGGACGCGGAGGAG 533
QY 2661 ACCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2720
DB 532 ----GACGAGGACGCGGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 477
QY 2721 CGACGT 2780
DB 476 CGAGGACGCGGAGGAG 417
QY 2781 CTGATGAGGCGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2840
DB 416 CGGGAGGAG 357
QY 2841 GTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2900
DB 356 GAGAGGAGGAG 297
QY 2901 GCGCGGCGCGGAGATGCTGCGGCGAGAGAGCTGCGCG 2937
DB 296 GAGCGGAGGAGGAG 260

RESULT 14
US-10-237-551-193/c
Sequence 193, Application US/10237551
Patent No. 6821519
GENERAL INFORMATION:
APPLICANT: Day, Craig H.
APPLICANT: Hosken, Nancy A.
APPLICANT: Parsons, Joseph M.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND
TITLE OF INVENTION: TREATMENT OF HERPES SIMPLEX VIRUS INFECTION
FILE REFERENCE: 210121.538C3
CURRENT APPLICATION NUMBER: US/10/237,551
NUMBER OF SEQ ID NOS: 254
SOFTWARE: PatSeq for Windows Version 4.0
SEQ ID NO 193
LENGTH: 3957
TYPE: DNA
ORGANISM: HSV2

US-10-237-551-193
Query Match 1.5%; Score 58.6; DB 4; Length 3957;
Best Local Similarity 50.1%; Pred. No. 0.00028;
Matches 171; Conservative 0; Mismatches 169; Indels 1; Gaps 1;

QY 2247 GCGGCGGAG 2306
DB 1955 GCCAGGCGCTTCCAGAGATCCCGCGGAGGCGGCGGAGAGAGAGAGAGAGAGAGAGAGAG 1896
QY 2307 TTGATGATGCGCGGCGGAG 2366
DB 1895 TCCG 1836
QY 2367 ATGTCCACCCCGGAG 2426
DB 1835 CCGGCGCGGAG 1776
QY 2427 CCGCGCGGAG 2486
DB 1775 GCGCGGTAGCCCGCGGAG 1716
QY 2487 GCGTTCG 2546
DB 1715 G-GGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 1657
QY 2547 CTGTGTACCTTCCAGCGCTGT 2587
DB 1656 GCGGCGGT 1616

RESULT 15
US-09-827-688-8
Sequence 8, Application US/09827688
Patent No. 6821955
GENERAL INFORMATION:
APPLICANT: ORSON, FRANK
APPLICANT: KINSLEY, BERNIA
APPLICANT: BHOGLI, BALBIR
TITLE OF INVENTION: MACROAGGREGATED PROTEIN CONJUGATES AS ORAL GENETIC IMMUNIZATION
TITLE OF INVENTION: AGENTS
FILE REFERENCE: P01949US/1/0004014
CURRENT APPLICATION NUMBER: US/09/827,688
PRIOR FILING DATE: 2001-04-06
PRIOR APPLICATION NUMBER: 60/195,680
NUMBER OF SEQ ID NOS: 13
SOFTWARE: PatentIn version 3.0
SEQ ID NO 8
LENGTH: 154746
TYPE: DNA
ORGANISM: HERPESVIRUS 2
US-09-827-688-8

Query Match 1.5%; Score 58.6; DB 4; Length 154746;
Best Local Similarity 50.1%; Pred. No. 0.0026;
Matches 171; Conservative 0; Mismatches 169; Indels 1; Gaps 1;

QY 2247 GCGGCGGAG 2306
DB 130078 GCCAGGCGCTTCCAGAGATCCCGGCGGAGGCGGCGGAGAGAGAGAGAGAGAGAGAGAGAG 130137
QY 2307 TTGATGATGCGCGGCGGAG 2366
DB 130138 TCCG 130197
QY 2367 ATGTCCACCCCGGAG 2426
DB 130198 CCGGCGGAG 130257
QY 2427 CCGGCGGAG 2486
DB 130258 GCGGCGGTAGCCCGCGGAG 130317

Qy 2487 GCGTTGCGCGCGCGCGGCGAGTTGCGGGGCTCCTCACTTACGACAGCCTCGGCAAG 2546
Db 130318 G-GGCGGCGCGCGCGCGGACTTCCCGCGGCGTGTGCGCGTTGGCGTC 130376
Qy 2547 CTGATCTTACCTTCCACGCGCTGCGTCAACCGAGACGCTCGCCT 2587
Db 130377 GCCGCCGTGTCGCGGGGTTGCGCGCCCGGTCAAGCGCCGCGT 130417

Search completed: September 24, 2005, 13:13:45
Job time : 606 secs